

GenCore version 5.1.6
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W protein - protein search, using sw model

run on: March 15, 2004, 07:25:43 ; Search time 60 Seconds
(without alignments)

1125.481 Million cell updates/sec

Title: US-09-620-955b-6

Perfect score: 1250
Sequence: 1 QVQLQESGGGLVQPGGSLRL.....CSFANSGLPLGGGRTVTYL 239

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_29Jan04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	1250	100.0	239	4	AAB69603	Huntingt1	AAB69603 Huntingt1
2	1110	88.8	254	5	ABP44972	Human Bly	ABP44972 Human Bly
3	1106	88.5	256	5	ABP44828	Human Bly	ABP44828 Human Bly
4	1097	87.8	252	5	ABP45616	Human Bly	ABP45616 Human Bly
5	1096	87.7	254	5	ABP44970	Human Bly	ABP44970 Human Bly
6	1095.5	87.6	241	5	ABP46044	Human Bly	ABP46044 Human Bly
7	1093	87.4	252	5	ABP44945	Human Bly	ABP44945 Human Bly
8	1089.5	87.2	251	5	ABP44944	Human Bly	ABP44944 Human Bly
9	1089.5	87.2	251	5	ABP45306	Human Bly	ABP45306 Human Bly
10	1088.5	87.1	251	5	ABP45103	Human Bly	ABP45103 Human Bly
11	1084.5	86.8	253	5	ABP44992	Human Bly	ABP44992 Human Bly
12	1082.5	86.6	251	5	ABP45321	Human Bly	ABP45321 Human Bly
13	1079	86.3	254	5	ABP45690	Human Bly	ABP45690 Human Bly
14	1079	86.3	254	5	ABP45748	Human Bly	ABP45748 Human Bly
15	1078	86.2	256	5	ABP45381	Human Bly	ABP45381 Human Bly
16	1077.5	86.2	253	5	ABP44978	Human Bly	ABP44978 Human Bly
17	1077	86.2	254	5	ABP44870	Human Bly	ABP44870 Human Bly
18	1073.5	85.9	253	5	ABP44996	Human Bly	ABP44996 Human Bly
19	1072	85.8	244	5	ABP45899	Human Bly	ABP45899 Human Bly
20	1067	85.4	254	5	ABP44966	Human Bly	ABP44966 Human Bly
21	1065	85.2	240	5	ABP46036	Human Bly	ABP46036 Human Bly
22	1065	85.2	254	5	ABP45417	Human Bly	ABP45417 Human Bly
23	1064.5	85.2	253	5	ABP45438	Human Bly	ABP45438 Human Bly
24	1063	85.0	254	5	ABP45064	Human Bly	ABP45064 Human Bly
25	1062	85.0	254	5	ABP45724	Human Bly	ABP45724 Human Bly

ALIGNMENTS

RESULT 1
AAB69603
ID AAB69603 standard; protein; 239 AA.

XX AAB69603;

XX DT 30-APR-2001 (first entry)

XX DE Huntingtin intrabody alpha-Nt-HD-C4 sFV.

XX KW Neurological disorder; Huntington's disease; Alzheimer's disease;
KW Parkinson's disease; prion disease; frontotemporal dementia;
KW amyotrophic lateral sclerosis; spinal and bulbar muscular atrophy;
KW dentatorubral-pallidoluysian atrophy; spinocerebellar ataxia type 1; SCA2;
KW SCA3; SCA4; SCA5; SCA6; SCA7; protein accumulation; intrabody.

XX OS Unidentified.

XX PN WO200106989-A2.

XX PD 01-FEB-2001.

XX PF 24-JUL-2000; 2000WO-US020131.

XX PR 27-JUL-1999; 99US-0146047P.

XX PR 21-JUL-2000; 2000US-00620955.

XX PA (HUST/) HUSTON J S.

XX PA (MESS/) MESSER A.

XX PA (LECE/) LECERF J.

XX PI Huston JS, Messer A, Lecerf J;

XX WPI; 2001-182700/18.

XX N-PSDB; AAF58707.

XX PT Inhibiting intracellular polypeptide accumulation, useful for treating
XX neurological disorders, e.g. Alzheimer's disease, comprises contacting
XX the polypeptide with a specific intrabody.

XX Claim 22; Page 95; 109pp; English.

XX The present invention describes a method for inhibiting the formation of
XX aggregates of certain proteins, involving contacting the protein with a
XX binding molecule known as an intrabody. Proteins to be bound include
XX those associated with neurological disorders, and so the method can be
XX used in the prevention of diseases such as Alzheimer's, Parkinson's and
XX Huntington's diseases, prion diseases, frontotemporal dementia,

ABP45594 Human Bly
ABP45326 Human Bly
ABP45303 Human Bly
ABP45662 Human Bly
ABP45887 Human Bly
ABP45420 Human Bly
ABP45679 Human Bly
ABP45919 Human Bly
ABP45313 Human Bly
ABP44872 Human Bly
ABP46066 Human Bly
ABP44984 Human Bly
ABP44904 Human Bly
ABP45623 Human Bly
ABP45771 Human Bly
Aao31142 Human Bly
ABP45642 Human Bly
ABP44914 Human Bly
ABP45808 Human Bly

26 1061.5 84.9 251 S ABP45594
27 1061.5 84.9 253 S ABP45326
28 1061 84.9 246 S ABP45303
29 1061 84.9 254 S ABP45662
30 1058 84.6 240 S ABP45887
31 1057 84.6 252 S ABP45420
32 1056 84.5 252 S ABP45679
33 1055 84.4 240 S ABP45919
34 1055 84.4 246 S ABP45313
35 1055 84.4 250 S ABP44872
36 1053 84.2 246 S ABP46066
37 1052.5 84.2 243 S ABP44984
38 1052.5 84.2 247 S ABP44904
39 1052 84.2 252 S ABP45623
40 1051 84.1 248 S ABP45771
41 1050.5 84.0 247 S Aao31142
42 1050.5 84.0 247 S ABP45642
43 1050 84.0 248 S ABP45642
44 1049.5 84.0 251 S ABP44914
45 1045.5 83.6 255 S ABP45808

CC amyotrophic lateral sclerosis, spinal and bulbar muscular atrophy,
 CC dentatorubral-pallidoluysian atrophy, spinocerebellar ataxia type 1
 CC (SCA1), SCA2, SCA3, SCA4, SCA5, SCA6 and SCA7
 XX Sequence 239 AA;
 SQ

Query Match 100.0%; Score 1250; DB 4; Length 239;
 Best Local Similarity 100.0%; Pred. No. 6.9e-81;
 Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSYSSMSVWRQAPGKLEWAVISYDGSNKYY 60
 DB 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSYSSMSVWRQAPGKLEWAVISYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRADETAVYICARDRYFDLWGRGTLVTVSSGGGGS 120
 DB 61 ADSVKGRFTISRDNKNTLYLQWNSLRADETAVYICARDRYFDLWGRGTLVTVSSGGGGS 120

QY 121 GGGGGGGGSSALTPQASVSGSPQSIITISCTGTSDDIGAYNVVSWYQYPGKAPKLLI 180
 DB 121 GGGGGGGGSSALTPQASVSGSPQSIITISCTGTSDDIGAYNVVSWYQYPGKAPKLLI 180

QY 181 YDVSNRPGISNRPFGSGSGDTASLTISGLQAEADYICSSFNANSGPLFGGSKTVTL 239
 DB 181 YDVSNRPGISNRPFGSGSGDTASLTISGLQAEADYICSSFNANSGPLFGGSKTVTL 239

RESULT 2
 ABP44972
 ID ABP44972 standard; protein; 254 AA.
 XX
 AC ABP44972;
 XX
 DT 19-AUG-2002 (first entry)
 DE Human Blys binding scFv SEQ ID 983.
 XX
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 XN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 XX
 PR 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAME-) CAMERIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX
 DR WPI; 2002-114799/15.
 XX
 PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX
 PS Claim 1; Page 1574-1575; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell

CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX Sequence 254 AA;
 SQ

Query Match 88.8%; Score 1110; DB 5; Length 254;
 Best Local Similarity 84.2%; Pred. No. 6.1e-71;
 Matches 213; Conservative 14; Mismatches 12; Indels 14; Gaps 2;

QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSYSSMSVWRQAPGKLEWAVISYDGSNKYY 60
 DB 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSYSSMSVWRQAPGKLEWAVISYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRADETAVYICARDRYFDLWGRGTLVTVSSGGGGS 120
 DB 61 ADSVKGRFTISRDNKNTLYLQWNSLRADETAVYICARDRYFDLWGRGTLVTVSSGGGGS 120

QY 108 GTLVTVSSGGGSGGSSALTPQASVSGSPQSIITISCTGTSDDIGAYNVVSW 167
 DB 121 GTLVTVSSGGGSGGSSALTPQASVSGSPQSIITISCTGTSDDIGAYNVVSW 180

QY 168 YQYVPGKAPKLLIYDVSNRPGISNRPFGSGSGDTASLTISGLQAEADYICSSFNANSG 226
 DB 181 YQYVPGKAPKLLIYDVSNRPGISNRPFGSGSGDTASLTISGLQAEADYICSSFNANSG 240

QY 227 GPLFGGSKTVTL 239
 DB 241 TRVFGSGTKTVL 253

RESULT 3
 ABP44828
 ID ABP44828 standard; protein; 256 AA.
 XX
 AC ABP44828;
 XX
 DT 19-AUG-2002 (first entry)
 DE Human Blys binding scFv SEQ ID 839.
 XX
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 XN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 PR 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX

2A	(HUMA-) HUMAN GENOME SCI INC.	XX
2A	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.	OS
2A	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;	XX
2A	WPI; 2002-114799/15.	XX
2A	Antibodies against B Lymphocyte Stimulating polypeptides, useful for the	PN
2A	diagnosis and treatment of cancers and immune disorders.	XX
2A	Claim 1; Page 1402-1403; 3148pp; English.	PD
2A	This invention describes novel antibodies that immunospecifically bind to	XX
2A	B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the	PF
2A	tumour necrosis factor (TNF) super family and induces B cell	XX
2A	proliferation and differentiation. The antibodies of the invention have	PR
2A	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,	PR
2A	anti-rheumatic and anti-AIDS activity and can be used in vaccines to	XX
2A	inhibit the expression and activity of Blys. The antibodies bind to Blys	XX
2A	and so may be used to detect and quantitate the presence of Blys in	PA
2A	biological samples and may be used in this way to diagnose disease	PA
2A	associated with aberrant expression of Blys. They may also be	PI
2A	administered to treat diseases associated with aberrant Blys expression	XX
2A	and activity such as cancer, immune, and autoimmune disorders and	XX
2A	diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,	XX
2A	immunodeficiency (e.g. common variable immunodeficiency (CVID) and	XX
2A	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent	PS
2A	the antibodies and fragments of the antibodies described in the method of	CC
2A	the invention	CC
2A	Sequence 256 AA;	XX
2A	Query Match 88.5%; Score 1106; DB 5; Length 256;	XX
2A	Best Local Similarity 83.9%; Pred. No. 1.2e-70;	CC
2A	Matches 213; Conservative 12; Mismatches 13; Indels 16; Gaps 2;	CC
2A	2 VOLQESGGGLVQPGSLRLSCAASGFTSSYSMSWVRQAPGKLEWVAIVSYDGSNKYYA 61	CC
2A	2 VOLQESGGGVVQPGSLRLSCAASGFTSSYSMSWVRQAPGKLEWVAIVSYDGSNKYYA 61	CC
2A	62 DSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCARDR-----YFDLWG 106	CC
2A	62 DSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCARDREAYVDILTYLYYYNDWG 121	CC
2A	107 RGLTVTVSSGGGGGGGGGGGGGQSALTPASVSGSGSITICTGTSSDYGNYYS 166	CC
2A	122 RGLTVTVSSGGGGGGGGGGGGGQSALTPASVSGSGSITICTGTSSDYGNYYS 181	CC
2A	167 WYQHPGKAPKLLIYDVSNRPSGINSRPSGSGDTSASLTISGLQAEADYVCSF-AN 225	CC
2A	182 WYQHPGKAPKLLIYDVSNRPSGINSRPSGSGDTSASLTISGLQAEADYVCSF-AN 241	CC
2A	226 SGLPFGGKTKTVL 239	CC
2A	242 STRVFGGKTKTVL 255	CC
2A	RESULT 4	CC
2A	ABP45616	XX
2A	ID ABP45616 standard; protein; 252 AA.	XX
2A	AC ABP45616;	XX
2A	DT DT	XX
2A	DE DE	XX
2A	19-AUG-2002 (first entry)	XX
2A	Human Blys binding scFv SEQ ID 1627.	XX
2A	Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;	XX
2A	tumour necrosis factor; B cell proliferation; B cell differentiation;	XX
2A	immunosuppressive; immunostimulant; immunomodulatory; anti-rheumatic;	XX
2A	anti-AIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;	XX
2A	systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;	XX
2A	common variable immunodeficiency; acquired immunodeficiency syndrome.	XX

RESULT 5

C the invention
X Q Sequence 241 AA;
Query Match 87.6%; Score 1095.5; DB 5; Length 241;
Best Local Similarity 86.2%; Pred. No. 6.2e-70;
Matches 207; Conservative 16; Mismatches 16; Indels 1; Gaps 1;
Y 1 QVQLQESGGGLVQPGGSLRLSQAASGFTFSYMSWVRQAPGKLEWVAIVSYDGNKYY 60
b 1 QVQLVQSGGDEVQPGSRRLSQAASGFTFSYMSWVRQAPGKLEWVAIVSYDGNKYY 60
Y 61 ADSVKGRTTISRDNKNTLYLQMSLRADTAIVYCARDRYDLWGRTGLVTVTSSGGGGS 120
b 61 ADSVKGRTTISRDNKNTLYLQMSLRADTAIVYCARDRYDLWGRTGLVTVTSSGGGGS 120
Y 121 GGGGSGGGGSGSALTQPSVSGSPGQSITISCTGTSSDIGAYNTVSYQYQPKAPKLLI 180
b 121 GGGGSGGGGSGSALTQPPSASGSPGQSITISCTGTSSDVGYNTVSYQYQHPKAPKEMI 180
Y 181 YDVSNRPISGNRFPSSGSGSDTASLTISGLQAEADYCYSSPAN-SGPIFGGGTKVTVL 239
b 181 YDVSKRPSGVNRPFGSGSGNTASLTISGLQAEADYCYSSYTSASTVIFGGGTKLTVL 240
RESULT 7
ID ABP44945 standard; protein; 252 AA.
AC ABP44945;
X 19-AUG-2002 (first entry)
DE Human BlyS binding scFv SEQ ID 956.
X BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
X tumour necrosis factor; B cell proliferation; B cell differentiation;
X immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
X anti-AIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
X systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
X common variable immunodeficiency; acquired immunodeficiency syndrome.
X Homo sapiens.
X WO200202641-A1.
X 10-JAN-2002.
X 15-JUN-2001; 2001WO-US019110.
X 16-JUN-2000; 2000US-0212210P.
X 17-OCT-2000; 2000US-0240816P.
X 16-MAR-2001; 2001US-0276249P.
X 21-MAR-2001; 2001US-0277379P.
X 25-MAY-2001; 2001US-0293499P.
X (HUMA-) HUMAN GENOME SCI INC.
X (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
X Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
X WPI; 2002-114799/15.
X Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
X diagnosis and treatment of cancers and immune disorders.
X Claim 1; Page 1542-1543; 3148pp; English.
X This invention describes novel antibodies that immunospecifically bind to
X B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
X tumour necrosis factor (TNF) super family and induces B cell
X proliferation and differentiation. The antibodies of the invention have
X cytostatic, immunosuppressive, immunostimulant, immunomodulatory, PA

CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
CC and so may be used to detect and quantitate the presence of BlyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BlyS. They may also be
CC administered to treat diseases associated with aberrant BlyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX Sequence 252 AA;
SQ Query Match 87.4%; Score 1093; DB 5; Length 252;
Best Local Similarity 84.1%; Pred. No. 9.8e-70;
Matches 211; Conservative 12; Mismatches 16; Indels 12; Gaps 2;
QY 1 QVQLQESGGGLVQPGGSLRLSQAASGFTFSYMSWVRQAPGKLEWVAIVSYDGNKYY 60
Db 1 QVQLVESGGGVQPGGSLRLSQAASGFTFSYMSWVRQAPGKLEWVAIVSYDGSDDKY 60
QY 61 ADSVKGRTTISRDNKNTLYLQMSLRADTAIVYCARDRYDLWGRTGLVTVTSSGGGGS 109
Db 61 EDSVKGRTTISRDNKNTLYLQMSLRADTAIVYCARDRYDLWGRTGLVTVTSSGGGGS 120
QY 110 LVTVSSGGGSGGGGSGSALTQPSVSGSPGQSITISCTGTSSDIGAYNTVSYQY 169
Db 121 TVTVSSGGGSGGGGSGSALTQPSVSGSPGQSITISCTGTSSDVGYNTVSYQY 180
QY 170 QYQKAPKLLIYDVSNRPISGNRFPSSGSGSDTASLTISGLQAEADYCYSSP-ANSGP 228
Db 181 QHPGKAPKLLIYEGSRPSPGVNRPFGSGSGNTASLTISGLQAEADYCYSSYTSSTR 240
QY 229 LFGGGTKVTVL 239
Db 241 VFGGGTKLTVL 251
RESULT 8
ID ABP44944 standard; protein; 251 AA.
AC ABP44944;
X 19-AUG-2002 (first entry)
DE Human BlyS binding scFv SEQ ID 955.
X BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
X tumour necrosis factor; B cell proliferation; B cell differentiation;
X immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
X anti-AIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
X systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
X common variable immunodeficiency; acquired immunodeficiency syndrome.
X Homo sapiens.
X WO200202641-A1.
X 10-JAN-2002.
X 15-JUN-2001; 2001WO-US019110.
X 16-JUN-2000; 2000US-0212210P.
X 17-OCT-2000; 2000US-0240816P.
X 16-MAR-2001; 2001US-0276249P.
X 21-MAR-2001; 2001US-0277379P.
X 25-MAY-2001; 2001US-0293499P.
X (HUMA-) HUMAN GENOME SCI INC.
X (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY. PA

XX FI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX DR WPI; 2002-114799/15.
XX PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX PT diagnosis and treatment of cancers and immune disorders.
XX PS Claim 1; Page 1541-1542; 3148pp; English.
XX CC This invention describes novel antibodies that immunospecifically bind to
CC CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC CC tumour necrosis factor (TNF) super family and induces B cell
CC CC proliferation and differentiation. The antibodies of the invention have
CC CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC CC and so may be used to detect and quantitate the presence of Blys in
CC CC biological samples and may be used in this way to diagnose disease
CC CC associated with aberrant expression of Blys. They may also be
CC CC administered to treat diseases associated with aberrant Blys expression
CC CC and activity such as cancer, immune, and autoimmune disorders and
CC CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC CC the antibodies and fragments of the antibodies described in the method of
CC CC the invention
XX SQ Sequence 251 AA;
Query Match 87.2%; Score 1089.5; DB 5; Length 251;
Best Local Similarity 83.6%; Pred. No. 1.7e-69;
Matches 209; Conservative 14; Mismatches 16; Indels 11; Gaps 2;
QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 1 EVQLVESGGGVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKLEWVAIVSYDGSNKYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARDR-----YFDLWGRGTL 110
Db 61 ADSVKGRFTVSRDNKNTLYLQMSLRADTAIVYCARDR-----YFDLWGRGTL 120
QY 111 VTVSSGGGGSGGGGGGQSALTQPASVSGSGPQSITISCTGTSDDIGAYNVSWYQQ 170
Db 121 VTVSSGGGGSGGGGGGQSALTQPASVSGSGPQSITISCTGTSDDIGAYNVSWYQQ 180
QY 171 YPGKAPKLLIYDVSNRPGISNRFSGSKSGTASLTISGLQAEDEADYYCSSF-ANSGPL 229
Db 181 HPGKAPKLLIYEGSRKPGVSNRFGSGSKSGNTASLTISGLQAEDEADYYCSYTRSTRV 240
RESULT 9
ABP45306 standard; protein; 251 AA.
XX AC ABP45306;
XX DT 19-AUG-2002 (first entry)
XX DE Human Blys binding scFv SEQ ID 1317.
XX KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW artAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX OS Homo sapiens.

XX PN WO200202641-A1.
XX PD 10-JAN-2002.
XX XX 15-JUN-2001; 2001WO-US019110.
XX PF 16-JUN-2000; 2000US-0212210P.
XX PR 17-OCT-2000; 2000US-0240816P.
XX PR 16-MAR-2001; 2001US-0276248P.
XX PR 21-MAR-2001; 2001US-027379P.
XX PR 25-MAY-2001; 2001US-0293499P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
DR WPI; 2002-114799/15.
XX PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX PT diagnosis and treatment of cancers and immune disorders.
XX PS Claim 1; Page 1974-1975; 3148pp; English.
XX CC This invention describes novel antibodies that immunospecifically bind to
CC CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC CC tumour necrosis factor (TNF) super family and induces B cell
CC CC proliferation and differentiation. The antibodies of the invention have
CC CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC CC and so may be used to detect and quantitate the presence of Blys in
CC CC biological samples and may be used in this way to diagnose disease
CC CC associated with aberrant expression of Blys. They may also be
CC CC administered to treat diseases associated with aberrant Blys expression
CC CC and activity such as cancer, immune, and autoimmune disorders and
CC CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC CC the antibodies and fragments of the antibodies described in the method of
CC CC the invention
XX SQ Sequence 251 AA;
Query Match 87.2%; Score 1089.5; DB 5; Length 251;
Best Local Similarity 83.6%; Pred. No. 1.7e-69;
Matches 209; Conservative 14; Mismatches 16; Indels 11; Gaps 2;
QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 1 QITLKEGGGVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKLEWVAIVSYDGSNKYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARDR-----YFDLWGRGTL 110
Db 61 ADSVKGRFTVSRDNKNTLYLQMSLRADTAIVYCARDR-----YFDLWGRGTL 120
QY 111 VTVSSGGGGSGGGGGGQSALTQPASVSGSGPQSITISCTGTSDDIGAYNVSWYQQ 170
Db 121 VTVSSGGGGSGGGGGGQSALTQPASVSGSGPQSITISCTGTSDDIGAYNVSWYQQ 180
QY 171 YPGKAPKLLIYDVSNRPGISNRFSGSKSGTASLTISGLQAEDEADYYCSSF-ANSGPL 229
Db 181 HPGKAPKLLIYEGSRKPGVSNRFGSGSKSGNTASLTISGLQAEDEADYYCSYTRSTRV 240
RESULT 10
ABP45103 standard; protein; 251 AA.
ID ABP45103

X DB ABP45103;
X 19-AUG-2002 (first entry)
X Human BlyS binding scFv SEQ ID 1114.
X BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
W tumour necrosis factor; B cell proliferation; B cell differentiation;
W immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
W antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
W systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
W common variable immunodeficiency; acquired immunodeficiency syndrome.
X Homo sapiens.
X ABP44992 standard; protein; 253 AA.
X WO200202641-A1.
X 10-JAN-2002.
X 15-JUN-2001; 2001WO-US019110.
X 15-JUN-2000; 2000US-0212210P.
X 17-OCT-2000; 2000US-0240816P.
X 16-MAR-2001; 2001US-0276248P.
X 21-MAR-2001; 2001US-0277379P.
X 25-MAY-2001; 2001US-0293499P.
X (HUMA-) HUMAN GENOME SCI INC.
X (CAMS-) CAMBRIDGE ANTIBODY TECHNOLOGY.
X Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
X WPI; 2002-114799/15.
X Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
X diagnosis and treatment of cancers and immune disorders.
X Claim 1; Page 1731-1732; 3148pp; English.
X This invention describes novel antibodies that immunospecifically bind to
X B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
X tumour necrosis factor (TNF) super family and induces B cell
X proliferation and differentiation. The antibodies of the invention have
X cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
X antirheumatic and antiAIDS activity and can be used in vaccines to
X inhibit the expression and activity of BlyS. The antibodies bind to BlyS
X and so may be used to detect and quantitate the presence of BlyS in
X biological samples and may be used in this way to diagnose disease
X associated with aberrant expression of BlyS. They may also be
X administered to treat diseases associated with aberrant BlyS expression
X and activity such as cancer, immune, and autoimmune disorders and
X diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
X immunodeficiency (e.g. common variable immunodeficiency (CVID) and
X acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
X the antibodies and fragments of the antibodies described in the method of
X the invention
X Sequence 251 AA;
Query Match 87.1%; Score 1088.5; DB 5; Length 251;
Best Local Similarity 83.2%; Pred. No. 2e-69;
Matches 208; Conservative 16; Mismatches 15; Indels 11; Gaps 2;
QY 1 QVQLQESGGGLVQPGGSLRLSCAAGSFYSSYSNWRQAPGKLEWVNTSYDGSNKY 60
D 1 EVQLVESGGGVQPGGSLRLSCAAGFTVYAMHWVRQAPGKGLQWVAIVSYDGSKKY 60
QY 61 ADSVKGRFTISRDNSKNTLYLQWNSLRADTAIVYICARDR-----YFDLWGRGTL 110
D 61 ADSVKGRFTVSRDNSKNTLYLQWNSLRADTAIVYICARSHYDILTGLNYWYFDLWGGTT 120
QY 111 VTVSSGGGGGGGGGGGSGSALTPASVSGSPQSGITISCTGTSDDVGVYVSWYQQ 170

DB 121 VTVSSGGGGGGGGGGGSGSALTPASVSGSPQSGITISCTGTSDDVGVYVSWYQQ 180
QY 171 YPGKAPKLLIYDVSNRPSGINSRPSGSKGSDTASLTISGLQADEADYYCSSF-ANSGPL 229
D 181 HPGKAPKLLIYEGSKRPSGVSNRPSGSKGSDTASLTISGLQADEADYYCSSYTRSTRV 240
QY 230 FGGGKVTVL 239
D 241 FGGGKVTVL 250
RESULT 11
ABP44992
ID ABP44992 standard; protein; 253 AA.
X AC ABP44992;
X 19-AUG-2002 (first entry)
X Human BlyS binding scFv SEQ ID 1003.
X BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
W tumour necrosis factor; B cell proliferation; B cell differentiation;
W immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
W antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
W systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
W common variable immunodeficiency; acquired immunodeficiency syndrome.
X Homo sapiens.
X WO200202641-A1.
X 10-JAN-2002.
X 15-JUN-2001; 2001WO-US019110.
X 16-JUN-2000; 2000US-0212210P.
X 17-OCT-2000; 2000US-0240816P.
X 16-MAR-2001; 2001US-0276248P.
X 21-MAR-2001; 2001US-0277379P.
X 25-MAY-2001; 2001US-0293499P.
X (HUMA-) HUMAN GENOME SCI INC.
X (CAMS-) CAMBRIDGE ANTIBODY TECHNOLOGY.
X Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
X WPI; 2002-114799/15.
X Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
X diagnosis and treatment of cancers and immune disorders.
X Claim 1; Page 1598-1599; 3148pp; English.
X This invention describes novel antibodies that immunospecifically bind to
X B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
X tumour necrosis factor (TNF) super family and induces B cell
X proliferation and differentiation. The antibodies of the invention have
X cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
X antirheumatic and antiAIDS activity and can be used in vaccines to
X inhibit the expression and activity of BlyS. The antibodies bind to BlyS
X and so may be used to detect and quantitate the presence of BlyS in
X biological samples and may be used in this way to diagnose disease
X associated with aberrant expression of BlyS. They may also be
X administered to treat diseases associated with aberrant BlyS expression
X and activity such as cancer, immune, and autoimmune disorders and
X diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
X immunodeficiency (e.g. common variable immunodeficiency (CVID) and
X acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
X the antibodies and fragments of the antibodies described in the method of
X the invention

SQ Sequence 253 AA;
Query Match 86.8%; Score 1084.5; DB 5; Length 253;
Best Local Similarity 82.9%; Pred. No. 3.9e-69;
Matches 209; Conservative 14; Mismatches 16; Indels 13; Gaps 2;
QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKLEWVAIVSYDGSNKYY 60
DB 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKLEWVAIVSYDGSNKYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCARDPDI-----WGRG 108
DB 61 VDSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCARDPDI-----WGRG 108
QY 109 TLVTSSGGGGGGGGGGGGGSGGSGSALTQTPASVSGSPGQSITISCTGTSDDIGAYNTVSWY 168
DB 121 TLVTSSGGGGGGGGGGGGGSGGSGSALTQTPASVSGSPGQSITISCTGTSDDIGAYNTVSWY 180
QY 169 QVPEGKAPKLLIYDVSNRPSGISNRFSKSGSDTASLTISGLQAEDEADYVCSF-ANSG 227
DB 181 QVPEGKAPKLLIYDVSNRPSGISNRFSKSGSDTASLTISGLQAEDEADYVCSF-ANSG 240
QY 228 PLFGGGTKVTL 239
DB 241 RVFGGGTKVTL 252
RESULT 12
ABP45321
ID ABP45321 standard; protein; 251 AA.
XX AC ABP45321;
XX DT 19-AUG-2002 (first entry)
XX DE Human BlyS binding scFv SEQ ID 1332.
XX KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX OS Homo sapiens.
XX PN WO200202641-A1.
XX PD 10-JAN-2002.
XX PF 15-JUN-2001; 2001WO-US019110.
XX PR 16-JUN-2000; 2000US-0212210P.
XX PR 17-OCT-2000; 2000US-0240816P.
XX PR 16-MAR-2001; 2001US-0276248P.
XX PR 21-MAR-2001; 2001US-0277379P.
XX PR 25-MAY-2001; 2001US-0293499P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PB (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX DR
XX PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX PS Claim 1; Page 1992-1993; 3148pp; English.
XX CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell

CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
CC and so may be used to detect and quantitate the presence of BlyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BlyS. They may also be
CC administered to treat diseases associated with aberrant BlyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX Sequence 251 AA;
Query Match 86.6%; Score 1082.5; DB 5; Length 251;
Best Local Similarity 83.2%; Pred. No. 5.4e-69;
Matches 208; Conservative 14; Mismatches 17; Indels 11; Gaps 2;
QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKLEWVAIVSYDGSNKYY 60
DB 1 EVQLVQSGGGVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKLEWVAIVSYDGSNKYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCARDPDI-----YEDLWGRGTL 110
DB 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCARDPDI-----YEDLWGRGTL 120
QY 111 VTSSGGGGGGGGGGGGGSGGSGSALTQTPASVSGSPGQSITISCTGTSDDIGAYNTVSWY 170
DB 121 VTSSGGGGGGGGGGGGGSGGSGSALTQTPASVSGSPGQSITISCTGTSDDIGAYNTVSWY 180
QY 171 YPGKAPKLLIYDVSNRPSGISNRFSKSGSDTASLTISGLQAEDEADYVCSF-ANSGPL 229
DB 181 HPGKAPKLLIYDVSNRPSGISNRFSKSGSDTASLTISGLQAEDEADYVCSF-ANSGPL 240
QY 230 FGGGTRKTVL 239
DB 241 FGGGTRKTVL 250
RESULT 13
ABP45690
ID ABP45690 standard; protein; 254 AA.
XX AC ABP45690;
XX DT 19-AUG-2002 (first entry)
XX DE Human BlyS binding scFv SEQ ID 1701.
XX KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX OS Homo sapiens.
XX PN WO200202641-A1.
XX PD 10-JAN-2002.
XX PF 15-JUN-2001; 2001WO-US019110.
XX PR 16-JUN-2000; 2000US-0212210P.
XX PR 17-OCT-2000; 2000US-0240816P.
XX PR 16-MAR-2001; 2001US-0276248P.
XX PR 21-MAR-2001; 2001US-0277379P.
XX PR 25-MAY-2001; 2001US-0293499P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PB (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX DR
XX PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX PS Claim 1; Page 1992-1993; 3148pp; English.
XX CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell

(HUMA-) HUMAN GENOME SCI INC.
 (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 WPI; 2002-114799/15.
 Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 diagnosis and treatment of cancers and immune disorders.
 Claim 1; Page 2432-2433; 3148pp; English.
 This invention describes novel antibodies that immunospecifically bind to
 B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 tumour necrosis factor (TNF) super family and induces B cell
 proliferation and differentiation. The antibodies of the invention have
 cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 antirheumatic and antiAIDS activity and can be used in vaccines to
 inhibit the expression and activity of Blys. The antibodies bind to Blys
 and so may be used to detect and quantitate the presence of Blys in
 biological samples and may be used in this way to diagnose disease
 associated with aberrant expression of Blys. They may also be
 administered to treat diseases associated with aberrant Blys expression
 and activity such as cancer, immune, and autoimmune disorders and
 diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
 the antibodies and fragments of the antibodies described in the method of
 the invention
 Sequence 254 AA;
 Query Match 86.3%; Score 1079; DB 5; Length 254;
 Best Local Similarity 81.8%; Pred. No. 9.7e-69;
 Matches 207; Conservative 18; Mismatches 14; Indels 2;
 Gaps 2;
 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSYMSWVRQAPGKLEWAVISYDGSNKYY 60
 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSYMSWVRQAPGKLEWAVISYDGSNKYY 60
 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARDRYF-----DLWGR 107
 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARDRYF-----DLWGR 107
 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARDRYF-----DLWGR 107
 108 GTLVTVSSGGGGSGGGSGGSGQSALTPASVSGSPGQSITISCTGTSDDIGAYNVSW 167
 121 GTWTVSSGGGGSGGGSGGSGQSALTPASVSGSPGQSITISCTGTSDDIGAYNVSW 180
 168 YQOYPGKAPKLLIYDVSNRPSGISNRFSGSKSGDTSASLTISGLQADEADYICSSP-ANS 226
 181 YQOHPGKAPKLLIYDVSNRPSGISNRFSGSKSGDTSASLTISGLQADEADYICSSP-ANS 226
 227 GPLFGGKTKTVL 239
 241 TRVFGGKTKTVL 253
 RESULT 14
 ABP45748
 ID ABP45748 standard; protein; 254 AA.
 XX
 AC ABP45748;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human Blys binding scfv SEQ ID 1759.
 XX
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.
 OS WO200202641-A1.
 XX
 XX 10-JAN-2002.
 XX
 XX 15-JUN-2001; 2001WO-US019110.
 XX
 XX 16-JUN-2000; 2000US-0212210P.
 XX
 XX 17-OCT-2000; 2000US-0240816P.
 XX
 XX 16-MAR-2001; 2001US-0276248P.
 XX
 XX 21-MAR-2001; 2001US-0277379P.
 XX
 XX 25-MAY-2001; 2001US-0293499P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.
 XX
 XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 XX diagnosis and treatment of cancers and immune disorders.
 XX
 XX Claim 1; Page 2501-2502; 3148pp; English.
 XX
 XX This invention describes novel antibodies that immunospecifically bind to
 XX B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 XX tumour necrosis factor (TNF) super family and induces B cell
 XX proliferation and differentiation. The antibodies of the invention have
 XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 XX antirheumatic and antiAIDS activity and can be used in vaccines to
 XX inhibit the expression and activity of Blys. The antibodies bind to Blys
 XX and so may be used to detect and quantitate the presence of Blys in
 XX biological samples and may be used in this way to diagnose disease
 XX associated with aberrant expression of Blys. They may also be
 XX administered to treat diseases associated with aberrant Blys expression
 XX and activity such as cancer, immune, and autoimmune disorders and
 XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 XX acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
 XX the antibodies and fragments of the antibodies described in the method of
 XX the invention
 XX Sequence 254 AA;
 SQ
 Query Match 86.3%; Score 1079; DB 5; Length 254;
 Best Local Similarity 82.2%; Pred. No. 9.7e-69;
 Matches 208; Conservative 16; Mismatches 15; Indels 14; Gaps 2;
 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSYMSWVRQAPGKLEWAVISYDGSNKYY 60
 1 QVQLVQSGGIVQPGSLRLSCLASGFTFSYMSWVRQAPGKLEWAVISYDGSNKYY 60
 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARDRYF-----WGR 107
 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARDRYF-----WGR 107
 108 GTLVTVSSGGGGSGGGSGGSGQSALTPASVSGSPGQSITISCTGTSDDIGAYNVSW 167
 121 GTWTVSSGGGGSGGGSGGSGQSALTPASVSGSPGQSITISCTGTSDDIGAYNVSW 180
 168 YQOYPGKAPKLLIYDVSNRPSGISNRFSGSKSGDTSASLTISGLQADEADYICSSP-ANS 226
 181 YQOHPGKAPKLLIYDVSNRPSGISNRFSGSKSGDTSASLTISGLQADEADYICSSP-ANS 226
 227 GPLFGGKTKTVL 239
 241 TRVFGGKTKTVL 253
 RESULT 15

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DM protein - protein search, using sw model

Run on: March 15, 2004, 07:25:43 ; Search time 22 Seconds
(without alignments)
560.846 Million cell updates/sec

Title: US-09-620-955B-6
Perfect score: 1250
Sequence: 1 QVQLQSGGGLVPGGSLRL.....CSFSFANSGFLFGGKTIVTL 239

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTCUS COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	1015.5	81.2	310	4	US-09-079-029-11	Sequence 11, Appl
2	906	72.5	244	4	US-08-918-148-79	Sequence 79, Appl
3	902.5	72.2	312	4	US-09-079-029-10	Sequence 10, Appl
4	897.5	71.8	249	4	US-10-039-785-53	Sequence 53, Appl
5	860.5	68.8	249	4	US-08-918-148-74	Sequence 74, Appl
6	860	68.8	309	4	US-09-079-029-9	Sequence 9, Appl
7	855.5	68.4	334	4	US-09-646-028-53	Sequence 53, Appl
8	855.5	68.4	339	4	US-09-646-028-55	Sequence 55, Appl
9	855.5	68.4	348	4	US-09-646-028-51	Sequence 51, Appl
10	850.5	68.0	245	4	US-10-039-785-43	Sequence 43, Appl
11	839.5	67.2	245	4	US-10-039-785-47	Sequence 47, Appl
12	839.5	67.2	245	4	US-10-039-785-51	Sequence 51, Appl
13	838.5	67.1	245	4	US-08-918-148-75	Sequence 75, Appl
14	837.5	67.0	245	4	US-08-918-148-76	Sequence 76, Appl
15	836.5	66.9	245	4	US-08-918-148-78	Sequence 78, Appl
16	834.5	66.8	245	4	US-10-039-785-52	Sequence 52, Appl
17	830.5	66.4	245	4	US-10-039-785-46	Sequence 46, Appl
18	829.5	66.4	245	4	US-10-039-785-42	Sequence 42, Appl
19	829.5	66.4	245	4	US-10-039-785-45	Sequence 45, Appl
20	820.5	65.6	245	4	US-10-039-785-49	Sequence 49, Appl
21	817.5	65.4	280	3	US-09-260-527-1	Sequence 1, Appl
22	817.5	65.4	281	4	US-09-028-769B-178	Sequence 178, App
23	815	65.2	244	4	US-08-918-148-77	Sequence 77, Appl
24	808.5	64.7	245	4	US-10-039-785-48	Sequence 48, Appl
25	788.5	62.8	236	2	US-08-190-199A-65	Sequence 65, Appl
26	782	62.6	255	4	US-09-553-498-8	Sequence 8, Appl
27	782	62.6	255	4	US-09-618-869-8	Sequence 8, Appl

28	775.5	62.0	258	2	US-08-665-202-5	Sequence 5, Appl
29	775.5	62.0	258	4	US-09-315-574-5	Sequence 5, Appl
30	773.5	61.9	284	3	US-08-564-164A-2	Sequence 2, Appl
31	773	61.8	240	2	US-08-956-047-25	Sequence 25, Appl
32	770	61.6	301	2	US-08-661-052-14	Sequence 14, Appl
33	770	61.6	301	3	US-08-188-082-14	Sequence 14, Appl
34	770	61.6	301	4	US-09-364-088-14	Sequence 14, Appl
35	770	61.6	301	4	US-09-102-716-14	Sequence 16, Appl
36	770	61.6	553	2	US-08-661-052-16	Sequence 16, Appl
37	770	61.6	553	3	US-09-188-082-16	Sequence 16, Appl
38	770	61.6	553	4	US-09-364-088-16	Sequence 16, Appl
39	770	61.6	553	4	US-09-102-716-16	Sequence 10, Appl
40	757.5	60.6	282	2	US-08-860-174A-10	Sequence 148, App
41	754.5	60.4	240	1	US-08-488-113B-148	Sequence 148, App
42	754.5	60.4	240	1	US-08-477-494B-148	Sequence 148, App
43	754.5	60.4	240	2	US-08-646-360-148	Sequence 148, App
44	754.5	60.4	240	3	US-08-839-765-148	Sequence 148, App
45	754.5	60.4	240	3	US-09-136-389-148	Sequence 148, App

ALIGNMENTS

RESULT 1
US-09-079-029-11
; Sequence 11, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; Filing Date:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

Query Match 81.2%; Score 1015.5; DB 4; Length 310;
Best Local Similarity 80.7%; Pred. No. 1.1e-68;
Matches 197; Conservative 16; Mismatches 26; Indels 5; Gaps 2;

QY 1 QVQLQSGGGLVPGGSLRLCAASGFTFSSYSMSGVRQAPGKLEWAVISYDGSNKYY 60
DB 40 QVQLVSGGGLVPGGSLRLCAASGFTFSSYGMHWVRQAPGKLEWAGIFYDGNKYY 99
QY 61 ADSVKGRFTISRDNRSKNTLYLQNSLRADTAVTYICARDR---YFDLWGRGLTVTVSSGG 117

Db 100 ADVKGRFTISRDNSKNTLYLQNSLRADTAVYCARDRGYYNDVWGKTTTVSSGG 159
QY 118 GSGGGGGGQSALTQPAVSQSPGQITISCTGSSDYGANNYSWYQYQPGKAPK 177
Db 160 GSGGGGGGQSALTQPPSVSGAPGQRTISCTGRSSNIGAGHDVHWYQQLPGTAPK 219
QY 178 LLIYDVSNRPSGINSRFGSKSGDTSALTISGLQAEDEADYYCSSFANS--GPIFGGGTK 235
Db 220 LLIYDNRPSGVPDRFSGSRGTSASLTGLQAEDEADYYCQSDYSLRGSVFGGJK 279
QY 236 VTVL 239
Db 280 VTVL 283

RESULT 2
US-08-918-148-79
; Sequence 79, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT FILING DATE: 1997-08-25
; CURRENT APPLICATION NUMBER: US/08/918,148A
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 79
; LENGTH: 244
; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-79

Query Match 72.5%; Score 906; DB 4; Length 244;
Best Local Similarity 72.5%; Pred. No. 1.3e-60;
Matches 174; Conservative 24; Mismatches 40; Indels 2; Gaps 2;
QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFFSSYSMSWRQAPKGLWVAVISYDQSNKY 60
Db 3 QVQLQESGGGLVQPGGSLRLSCAASGFTFFSSYSMSWRQAPKGLWVAVISYDQSNKY 61
QY 61 ADSVKGRTISRDNSKNTLYLQNSLRADTAVYCARDRYFDLWGRGTLTVSSGGGS 120
Db 62 NPSLSRVTLISVDTSKQFSLKSSVTAADTAVYCARGFYFDVWGRGTMTVSSGGGS 121
QY 121 GGGGGGGGQSALTQPAVSQSPGQITISCTGSSDYGANNYSWYQYQPGKAPKLI 180
Db 122 GGGGGGGGQSALTQPPSVSGAPGQRTISCTGRSSNIGAGHDVHWYQQLPGTAPK 181
QY 181 YDVSNRPSGINSRFGSKSGDTSALTISGLQAEDEADYYCSSF--ANSGPLFGGKTVTL 239
Db 182 YEGSKRPSGNSRFGSKSGDTSALTISGLQAEDEADYYCSTVTRVFGGKTVTL 241

RESULT 3
US-09-079-029-10
; Sequence 10, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marechang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-079-029-10
Query Match 72.2%; Score 902.5; DB 4; Length 312;
Best Local Similarity 73.9%; Pred. No. 3.1e-60;
Matches 184; Conservative 20; Mismatches 30; Indels 15; Gaps 5;
QY 2 VQLQESGGGLVQPGGSLRLSCAASGFTFFSSYSMSWRQAPKGLWVAVISYDQSNKY 61
Db 41 VQLVESGGGLVQPGGSLRLSCAASGFTFFSSYSMSWRQAPKGLWVAVISYDQSEKIV 100
QY 62 DSVKGRFTISRDNSKNTLYLQNSLRADTAVYCARD-----RYFDLWGRGTLTV 112
Db 101 DSVKGRFTISRDNAKNSLYLQNSLRADTAVYCARDLLKVKSSSGWFDPMGRGTTVT 160
QY 113 VSSGGGGGGGSGGSGQSALTQPAVSQSPGQITISCTGSSDYGANNYSWYQY 172
Db 161 VSSGGGGGGGSGGSGGS--SELTQDPAVSVALGQTVAITCQGS--LRSY-YASWYQKP 216
QY 173 GKAPKLIYDVSNRPSGINSRFGSKSGDTSALTISGLQAEDEADYYCSSFANS--PLF 230
Db 217 GQAPVLIYGVKNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSNGHVV 276
QY 231 GGGTKTVTL 239
Db 277 GGGTKTVTL 285

RESULT 4
US-10-039-785-53
; Sequence 53, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807

;; PRIOR FILING DATE: 2001-09-21
;; PRIOR APPLICATION NUMBER: 60/309,176
;; PRIOR FILING DATE: 2001-08-02
;; PRIOR APPLICATION NUMBER: 60/294,981
;; PRIOR FILING DATE: 2001-06-04
;; PRIOR APPLICATION NUMBER: 60/293,473
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 66
;; SOFTWARE: Patent in Ver. 2.1
;; SEQ ID NO 53
;; LENGTH: 249
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: T1006F07 scFv
US-10-039-785-53

Query Match 71.8%; Score 897.5; DB 4; Length 249;
Best Local Similarity 72.1%; Pred. No. 5.6e-60;
Matches 181; Conservative 21; Mismatches 34; Indels 15; Gaps 4;
QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSVVRQAPGKGLEWAVISYDGSNKYY 60
DB 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYSMSVVRQAPGKGLEWVAISYDGSNKYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADDTAVYICARDRYF-----DLWGRGTL 110
DB 61 ADSVKGRFTISRDNKNTLYLQMSLRADDTAVYICAREPSPQMGHYSYGMVNGQGTW 120
QY 111 VTVSSGGGGGGGGGGGGGAS-QSALTQPASVSGSPQSIITISCTGTSDDIGAYNYVSYQ 169
DB 121 VTVSSGGGGGGGGGGGSAQSGLTQPPSVSVFQAARITCSG--DKLGDKYASWYQ 177
QY 170 QYFGKAPKLLIYDVNRPISGNRPSGSGSGTASLTISGLQAEADYVCSFANSFGP- 228
DB 178 QRPGQSPVLIYQDNKRPSGIPERFSGNSGNTATLKISGTQAMDEADYVCLAWDSADW 237
QY 229 LFGGGTKVTVL 239
DB 238 VFGGGTKVTVL 248

RESULT 5

US-08-918-148-74
;; Sequence 74, Application US/08918148A
;; Patent No. 6342220
;; GENERAL INFORMATION:
;; APPLICANT: Adams, Camellia
;; APPLICANT: W.
;; APPLICANT: Carter, Paul J.
;; APPLICANT: Fendly, Brian M.
;; APPLICANT: Gurney, Austin L.
;; TITLE OF INVENTION: Agonist Antibodies
;; FILE REFERENCE: P0979
;; CURRENT APPLICATION NUMBER: US/08/918,148A
;; CURRENT FILING DATE: 1997-08-25
;; NUMBER OF SEQ ID NOS: 79
;; SEQ ID NO 74
;; LENGTH: 249
;; TYPE: PRT
;; ORGANISM: artificial
US-08-918-148-74

Query Match 68.8%; Score 860.5; DB 4; Length 249;
Best Local Similarity 68.0%; Pred. No. 3.3e-57;
Matches 166; Conservative 33; Mismatches 40; Indels 5; Gaps 2;
QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSVVRQAPGKGLEWAVISYDGSNKYY 60
DB 3 QVQLQESGGEMKPKGSLKISCKGYSPATSWIGVRQMPFGKLEWVAIMYPGNSDTRH 62
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADDTAVYICAR-----DRYFDLWGRGTLVTVSSG 116

DB 63 NPSFEDQVTMSADTGTINTAYLQWSSLKASDRTAMYCARAGVAGGAFDLWGKGTWTVTVSSG 122
QY 117 GGGSGGGGGGGGGGGGSSALTPASVSGSPQSIITISCTGTSDDIGAYNYVSYQYVPGKAP 176
DB 123 GGGSGGGGGGGGGGGGSSVLTQPASVSGSPQSIITISCTGTSDDIGAYNYVSYQYVPGKAP 182
QY 177 KLLIYDVNRPISGNRPSGSGSGTASLTISGLQAEADYVCSFANSFG-PLFGGGTK 235
DB 183 KLLIYGNRPSGVPDRFSASKSGNTASLTISGLQAEADYVCSFAPPGLIIMFGGGTK 242
QY 236 VTVL 239
DB 243 LTVL 246

RESULT 6

US-09-079-029-9
;; Sequence 9, Application US/09079029
;; Patent No. 6342369
;; GENERAL INFORMATION:
;; APPLICANT: Adams, Camilla W.
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Chuntharapai, Anan
;; APPLICANT: Kim, Kyung J.
;; TITLE OF INVENTION: Apo-2 Receptor
;; NUMBER OF SEQUENCES: 14
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 1 DNA Way
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatIn (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/079,029
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Marschang, Diane L.
;; REGISTRATION NUMBER: 35,600
;; REFERENCE/DOCKET NUMBER: P1101R2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-5416
;; TELEFAX: 650/952-9881
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 309 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
US-09-079-029-9

Query Match 68.8%; Score 860; DB 4; Length 309;
Best Local Similarity 70.0%; Pred. No. 4.6e-57;
Matches 173; Conservative 29; Mismatches 33; Indels 12; Gaps 5;
QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSVVRQAPGKGLEWAVISYDGSNKYY 60
DB 40 EVQLVQSGGQVERPGGSLRLSCAASGFTFDDYGMVSRVQAPGKGLEWVSGINWNGSGTY 99
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADDTAVYICAR-----RDYFDLWGRGTLVTVS 114
DB 100 ADSVKGRFTISRDNKNTLYLQMSLRADDTAVYICAKILQAGRWTFDLWGRGTLVTVS 159
QY 115 GGGSGGGGGGGGGGGGSSALTPASVSGSPQSIITISCTGTSDDIGAYNYVSYQYVPGK 174
DB 160 GGGSGGGGGGGGGGGGSS-SELTQDPASVALGQTVRITCQGDS--LRSY-YASWYQKPGQ 215
QY 175 APKLLIYDVNRPISGNRPSGSGSGTASLTISGLQAEADYVCSFANSFG-PLFGG 232

Db 216 APVLVIYKNNRPSGIPDRFGSSGNTASLTITGAQAEADYVYCNRSDDSGHVVFG 275
QY 233 GTKVTVL 239
Db 276 GTKLTVL 282

RESULT 7
US-09-646-028-53
; Sequence 53, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-53

Query Match 68.4%; Score 855.5; DB 4; Length 334;
Best Local Similarity 69.0%; Pred. No. 1.1e-56;
Matches 171; Conservative 29; Mismatches 39; Indels 9; Gaps 4;
QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSVWRQAPGKLEWNAVVISYDGSNKYY 60
Db 80 EVQLLESGLVQSGGSLRLSCVASGLTSSAITWVRQAPGKLEWVSGISFGDTTYY 139
QY 61 ADSVKGRFTISRDNKNTLYLQMSLAEDTAVYYCARDR----YFDLWGRGTLTVSS- 115
Db 140 ADSVKGRFSASRDNSKNTVYLMNNLRPNDAVYFCANNQTNFCLDNWGQGLTVTVSSR 199
QY 116 GGGSGGGGGGG--GQSALTOPASVSGSGSDTASLTISGLQAEADYVY--CSSFANSGLPFG 173
Db 200 GGGSGGGGGGG--GQSALTOPASVSGSGSDTASLTISGLQAEADYVY--CSSFANSGLPFG 259
QY 174 KAPKLLIYDVNRPISNRPSGSGSDTASLTISGLQAEADYVY--CSSFANSGLPFG 231
Db 260 TAPKVLIIYNNRNPISNRPSGSGSDTASLTISGLQAEADYVY--CSSFANSGLPFG 319
QY 232 GGTKVTVL 239
Db 320 GGTKLTVL 327

RESULT 8
US-09-646-028-55
; Sequence 55, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 55
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-55

Query Match 68.4%; Score 855.5; DB 4; Length 339;
Best Local Similarity 69.0%; Pred. No. 1.1e-56;
Matches 171; Conservative 29; Mismatches 39; Indels 9; Gaps 4;
QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSVWRQAPGKLEWNAVVISYDGSNKYY 60
Db 85 EVQLLESGLVQSGGSLRLSCVASGLTSSAITWVRQAPGKLEWVSGISFGDTTYY 144
QY 61 ADSVKGRFTISRDNKNTLYLQMSLAEDTAVYYCARDR----YFDLWGRGTLTVSS- 115
Db 145 ADSVKGRFSASRDNSKNTVYLMNNLRPNDAVYFCANNQTNFCLDNWGQGLTVTVSSR 204
QY 116 GGGSGGGGGGG--GQSALTOPASVSGSGSDTASLTISGLQAEADYVY--CSSFANSGLPFG 173
Db 205 GGGSGGGGGGG--GQSALTOPASVSGSGSDTASLTISGLQAEADYVY--CSSFANSGLPFG 264
QY 174 KAPKLLIYDVNRPISNRPSGSGSDTASLTISGLQAEADYVY--CSSFANSGLPFG 231
Db 265 TAPKVLIIYNNRNPISNRPSGSGSDTASLTISGLQAEADYVY--CSSFANSGLPFG 324
QY 232 GGTKVTVL 239
Db 325 GGTKLTVL 332

RESULT 9
US-09-646-028-51
; Sequence 51, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-51

Query Match 68.4%; Score 855.5; DB 4; Length 348;
Best Local Similarity 69.0%; Pred. No. 1.1e-56;
Matches 171; Conservative 29; Mismatches 39; Indels 9; Gaps 4;
QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSVWRQAPGKLEWNAVVISYDGSNKYY 60
Db 94 EVQLLESGLVQSGGSLRLSCVASGLTSSAITWVRQAPGKLEWVSGISFGDTTYY 153
QY 61 ADSVKGRFTISRDNKNTLYLQMSLAEDTAVYYCARDR----YFDLWGRGTLTVSS- 115
Db 154 ADSVKGRFSASRDNSKNTVYLMNNLRPNDAVYFCANNQTNFCLDNWGQGLTVTVSSR 213
QY 116 GGGSGGGGGGG--GQSALTOPASVSGSGSDTASLTISGLQAEADYVY--CSSFANSGLPFG 173
Db 214 GGGSGGGGGGG--GQSALTOPASVSGSGSDTASLTISGLQAEADYVY--CSSFANSGLPFG 273

QY 174 KAPKLLIYDVSNRPSGIGNSRFGSGSGDTASLTISGLQAEDEADYY--CSSFANSGLFLG 231
DB 274 TAPKVLIVSNRPSGVDPDRFSGSGSGTSASLAIITGLQLEDEGTYYCQCNDLSLGNLFG 333
QY 232 GGTKVTVL 239
DB 334 GGTKLTVL 341

RESULT 10
US-10-039-785-43
; Sequence 43, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1014G03 scFv
US-10-039-785-43

Query Match 68.0%; Score 850.5; DB 4; Length 245;
Best Local Similarity 68.0%; Pred. No. 1.8e-56;
Matches 166; Conservative 30; Mismatches 43; Indels 5; Gaps 3;

QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSKSWVRQAPGKGLEWVAIVSYDGSNKYY 60
DB 1 EVQLVQSGAEVKMPASVLSRVSGDITFTAYFIHWVQAQPGQGLEWGWGWFNPISGTAGS 60
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADETAVYYCARDY---RYFDLWGRGTLTVVSSGG 117
DB 61 AEKFRGRVAMTRDTISITAYMELNRLTDDTAVYYCARQHRGNTFDPWGQGTLLTVVSSGG 120
QY 118 GSGGGGGGGGGS-QSALTQPASVSGSPQGSITISCTGSSDIGAYNVSVYQYPGKAP 176
DB 121 GSGGGGGGGGGSQAQSAQTQPASVSGSPQGSITISCTGSSDIGAYKXVSVYQYHPGKAP 180
QY 177 KLLIYDVSNRPSGIGNSRFGSGSGDTASLTISGLQAEDEADYYCSSFANSGLP-LFGGGTK 235
DB 181 KLIVIEVSNRPSGVSSRFGSGSGGTASLTISGLQADDEADYYCNSYQGYNTWVFGGGTK 240
QY 236 VTVL 239
DB 241 VTVL 244

RESULT 12
US-10-039-785-51
; Sequence 51, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550

RESULT 11
US-10-039-785-47
; Sequence 47, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1014B11 scFv
US-10-039-785-47

Query Match 67.2%; Score 839.5; DB 4; Length 245;
Best Local Similarity 65.2%; Pred. No. 1.2e-55;
Matches 159; Conservative 38; Mismatches 42; Indels 5; Gaps 3;

QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSKSWVRQAPGKGLEWVAIVSYDGSNKYY 60
DB 1 EVQLVQSGAEVKMPASVLSRVSGDITFTAYFIHWVQAQPGQGLEWGWGWFNPISGTAGS 60
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADETAVYYCARDY---FDLWGRGTLTVVSSGG 117
DB 61 PKFHRGRVAMTRDTISITAYMELNRLTASDITAYICARQHHNTFDPWGQGTLLTVVSSGG 120
QY 118 GSGGGGGGGGGS-QSALTQPASVSGSPQGSITISCTGSSDIGAYNVSVYQYPGKAP 176
DB 121 GSGGGGGGGGGSQAQSAQTQPASVSGSPQGSITISCTGSSDIGAYNVSVYQYHPGKAP 180
QY 177 KLLIYDVSNRPSGIGNSRFGSGSGDTASLTISGLQAEDEADYYCSSFANSGLP-LFGGGTK 235
DB 181 KLIVIEVSNRPSGVSSRFGSGSGGTASLTISGLQADDEADYYCNSYQGYNTWVFGGGTK 240
QY 236 VTVL 239
DB 241 LTVL 244

RESULT 12
US-10-039-785-51
; Sequence 51, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550

; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 51
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1015A07 scfV
US-10-039-785-51

Query Match 67.2%; Score 839.5; DB 4; Length 245;
Best Local Similarity 65.1%; Pred. No. 1.2e-55;
Matches 162; Conservative 38; Mismatches 34; Indels 15; Gaps 5;
QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSYSSMSVWVQAQPGKLEWVAVI-----SYDG 55
DB 1 EVQLVQSGEVEVKPPASVKVSKISGDSFTAYFHNLQAQEGEGLWGNFNPISGADS 60
QY 56 SNKYVADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVVYCARDY---FDLWGRGTLVT 112
DB 61 PKKFH-----GRVAMRTDTSISTAYMELTRLASDSDTAIYCARQHHNSNTEFDPWGQGLT 115
QY 113 VSSGGGGGGGGGGGGG--QSALTQPASVSGSPGSGITISCTGSSDYGAYNYVSWYQY 171
DB 116 VSSGGGGGGGGGGGGGQAQSLTQTPASMSGSPGSGITISCTGSSDVGYNVSWYQY 175
QY 172 PGKAPKLLIYVSNRPSGISNRFSGSKGSDTASLTISGLQAEDEADYYCSFANSGLP-LF 230
DB 176 PGKAPKLLIYVSNRPSGISNRFSGSKGSDTASLTISGLQAEDEADYYCSFANSGLP-LF 235
QY 231 GGGTKVTVL 239
DB 236 GGGTKVTVL 244

RESULT 13
US-08-918-148-75
; Sequence 75, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 75
; LENGTH: 245
; TYPE: PRT

; ORGANISM: artificial
US-08-918-148-75
Query Match 67.1%; Score 838.5; DB 4; Length 245;
Best Local Similarity 67.8%; Pred. No. 1.4e-55;
Matches 164; Conservative 27; Mismatches 44; Indels 7; Gaps 3;
QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSYSSMSVWVQAQPGKLEWVAVISYDGSNKYY 60
DB 3 EVQLVQSGGGLVQPGGSLRLSCAASGFTFSYSSMSVWVQAQPGKLEWVAVISYDGSNKYY 62
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVVYCARDY---YFDLWGRGTLVTYSSGG 117
DB 63 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVVYCARDY---YFDLWGRGTLVTYSSGG 122
QY 118 GSGGGGGGGGGGGG--QSALTQ-PASVSGSPGSGITISCTGSSDYGAYNYVSWYQYFGKAP 176
DB 123 GSGGGGGGGGGGGG--QSALTQ-PASVSGSPGSGITISCTGSSDYGAYNYVSWYQYFGKAP 179
QY 177 KLLIYVSNRPSGISNRFSGSKGSDTASLTISGLQAEDEADYYCSFANSGLPFGGKT 236
DB 180 KLLIYKASSLASGAPSRFSGSGGSDTFTLTISLQPDDEADYYCSFANSGLPFGGKT 239
QY 237 TVL 238
DB 240 EV 241

RESULT 14
US-08-918-148-76
; Sequence 76, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 76
; LENGTH: 245
; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-76

Query Match 67.0%; Score 837.5; DB 4; Length 245;
Best Local Similarity 67.1%; Pred. No. 1.7e-55;
Matches 163; Conservative 28; Mismatches 45; Indels 7; Gaps 3;
QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSYSSMSVWVQAQPGKLEWVAVISYDGSNKYY 60
DB 3 EVQLVQSGGGLVQPGGSLRLSCAASGFTFSYSSMSVWVQAQPGKLEWVAVISYDGSNKYY 62
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVVYCARDY---YFDLWGRGTLVTYSSGG 117
DB 63 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVVYCARDY---YFDLWGRGTLVTYSSGG 122
QY 118 GSGGGGGGGGGGGG--QSALTQ-PASVSGSPGSGITISCTGSSDYGAYNYVSWYQYFGKAP 176
DB 123 GSGGGGGGGGGGGG--QSALTQ-PASVSGSPGSGITISCTGSSDYGAYNYVSWYQYFGKAP 179
QY 177 KLLIYVSNRPSGISNRFSGSKGSDTASLTISGLQAEDEADYYCSFANSGLPFGGKT 236
DB 180 KLLIYKASSLASGAPSRFSGSGGSDTFTLTISLQPDDEADYYCSFANSGLPFGGKT 239
QY 237 TVL 239
DB 240 EIL 242

RESULT 15
JS-08-918-148-78
; Sequence 78, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 78
; LENGTH: 245
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; NAME/KEY: unknown
; LOCATION: 208
; OTHER INFORMATION: unknown amino acid
US-08-918-148-78

Query Match 66.9%; Score 836.5; DB 4; Length 245;
Best Local Similarity 68.2%; Pred No. 2e-55; 42; Indels 7; Gaps 3;
Matches 165; Conservative 28; Mismatches 42; Indels 7; Gaps 3;
QY 1 QVQLQESGGGLYQPGGSLRLSCAASGFTFSYSSMSWVRQAPGKGLEWVAVISYDGSNKYY 60
Db 3 QVQLVESGGGLVQPGGSLRLSCAASGFTFSYSSMSWVRQAPGKGLEWVAVISYDGSNKYY 62
QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRRAEDTAVYYCARDR--YFDLWGRGTLTVSSGG 117
Db 63 ADSVKGRFTISRDNKNTLYLQWNSLRRAEDTAVYYCARDRGTGMDWGRGTLTVSSGG 122
QY 118 GSGGGGGGGGSGQSALTO-PASVSGSPGQITISCTCTSSDIGAYNVSWYQYQPKAP 176
Db 123 GSGGGGGGGGSGKIQMTQSPSTLSASIGDRVTITCRASE--GIYHWLAWYQKPKAP 179
QY 177 KLLIYDVSNRPSGISNRFSGSKSGDTSITSLGQAEDEADYCVSSFANSGLPFGGKTV 236
Db 180 KLLIYKASSLASGAPSRFSGSGSDTFTYTISSLPDDFATYYCQYSNYPLETGGGTKL 239
QY 237 TV 238
Db 240 EI 241

Search completed: March 15, 2004, 07:26:21
Job time : 23 secs

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XM protein - protein search, using sw model

run on: March 15, 2004, 07:25:43 ; Search time 20 seconds
(without alignments)
1149.489 Million cell updates/sec

Title: US-09-620-955B-6

Perfect score: 1250

Sequence: 1 QVQLQESGGGLVQPGGSLRL.....CSSPANSQPLFGGKTKVTVL 239

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR78.*

1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	619	49.5	268	2 A56446	Ig heavy chain V r
2	589.5	47.2	249	2 S41374	single chain Fv an
3	549.5	44.0	140	2 S70442	Ig heavy chain pre
4	547	43.8	119	2 F36005	Ig heavy chain V r
5	546	43.7	121	2 G36005	Ig heavy chain V r
6	541	43.3	132	2 S31603	Ig heavy chain V r
7	540.5	43.2	233	2 JC5322	p53 specific singl
8	539.5	43.2	122	2 G36005	Ig heavy chain V r
9	539	43.1	134	2 S31679	Ig heavy chain V r
10	538	43.0	123	2 S38493	Ig heavy chain - h
11	537.5	43.0	114	2 S46391	Ig heavy chain V r
12	534.5	42.8	114	2 S46390	Ig heavy chain V r
13	534.5	42.8	118	2 S31116	Ig heavy chain - h
14	534.5	42.8	122	2 S31117	Ig heavy chain - h
15	533	42.6	111	2 PH1645	Ig heavy chain V r
16	533	42.6	121	2 S19666	Ig heavy chain V r
17	531.5	42.5	128	2 S48797	Ig heavy chain V r
18	531	42.5	133	2 A49028	Ig heavy chain V-I
19	529	42.3	135	2 S31598	Ig heavy chain V r
20	528	42.2	138	2 S31666	Ig heavy chain V r
21	526	42.1	130	2 S31601	Ig heavy chain V r
22	525.5	42.0	137	2 S31701	Ig heavy chain V r
23	521.5	41.7	139	2 S31674	Ig heavy chain V r
24	520.5	41.6	114	2 S46392	Ig heavy chain V r
25	520	41.6	119	2 S31107	Ig heavy chain - h
26	518.5	41.5	120	2 S31112	Ig heavy chain - h
27	518	41.4	119	2 S31108	Ig heavy chain - h
28	517.5	41.4	120	2 S48798	Ig heavy chain V r
29	517.5	41.4	147	2 I37780	Ig variable region

30	516	41.3	130	2 PL0098	Ig heavy chain pre
31	516	41.3	140	2 S31588	Ig heavy chain V r
32	515	41.2	119	2 D36005	Ig heavy chain V r
33	512.5	41.0	128	2 S26790	Ig heavy chain V r
34	511.5	40.9	141	2 S31669	Ig heavy chain V r
35	511	40.9	119	2 C36005	Ig heavy chain V r
36	509	40.7	109	2 PH1646	Ig heavy chain V r
37	508.5	40.7	124	2 S20782	Ig heavy chain V r
38	508	40.6	125	2 S30531	Ig heavy chain V r
39	507.5	40.6	122	1 M3HUAM	Ig heavy chain V-I
40	505.5	40.4	133	2 S31510	Ig heavy chain - h
41	505.5	40.4	136	2 S31587	Ig heavy chain V r
42	505	40.4	111	2 PH1643	Ig heavy chain V r
43	505	40.4	123	2 S31114	Ig heavy chain - h
44	504.5	40.4	108	2 PH1642	Ig heavy chain V r
45	503	40.2	117	2 S78486	Ig heavy chain V r

ALIGNMENTS

RESULT 1

A56446

Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C/Species: Mus musculus (house mouse)

C/Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C/Accession: A56446

R/Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995
A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical
A/Reference number: A56446; MUID:95229583; PMID:7713873

A/Accession: A56446

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-268 <TAN>

A/Cross-references: GB:U20617

C/Keywords: heterotetramer; immunoglobulin

Query Match 49.5%; Score 619; DB 2; Length 268;

Best Local Similarity 51.7%; Pred. No. 5.4e-36;

Matches 125; Conservative 34; Mismatches 75; Indels 8; Gaps 3;

QY	1	QVQLQESGGGLVQPGGSLRLSCAASGFTFSYSSMSVQRAPGKLEWVAIVSYDGSNKYY	60
DB	3	QVQLQESGAELVKGASVKLSCTTSGFNIKDTYMHVVKRPEQGLEWIGRIAPANGITKY	62
QY	61	ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCAR---	117
DB	63	DPKFOGKATIAADTSNTAYLQLSLTSEDVAVYCAR---	122
QY	118	GGSGGGSGGGSGSALSTQ-PASVSGSPGQSIT-SCGTGSDIGAYNYKVIQYQKAP	176
DB	123	GGSGGGSGGGSGSDIELTQSPAIMSASLGEKVTMCRASSS---	178
QY	177	KLLIYDVSNRPSGISNRPFGSGKSGDTSLTISGLQADEADYVCSFANSGLPGGQTKV	236
DB	179	KLVYVTHLPFGVPARFSGSGSNSLTITSSMEGDDATYYCQFTSPFTFGSGTKL	238

RESULT 2

S41374

single chain Fv antibody - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C/Accession: S41374

R/Artsenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A/Description: Construction and functional characterization of a single chain Fv antibody

A/Reference number: S41374

A:Accession: S41374
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-249 <ART>
A:Cross-references: EMBL:Z29480

Query Match 47.2%; Score 589.5; DB 2; Length 249;
Best Local Similarity 51.4%; Pred. No. 5.5e-34;
Matches 125; Conservative 35; Mismatches 76; Indels 4;
Gaps 4;
QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSYSSMSWVRQAPGKLEWVAVISYDGSNKYY 60
DB 1 QVQLQESGAEVLPFGASVKLSCTASGTFNPKDDYIHWVQRPEKGLWVAVIAPASGNVY 60
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARDR---YFDLWGRGTLTVSS 116
DB 61 VPRFQKAITATSTNTAYLLSSLTSEDYAVYCAARDLYISLGVWGGSTVTVSSR 120
QY 117 GGSQGGSGGGSGGSGGQALQTPASVSGSPQSGITTCGTSSDI--GAYNVVWYQYPG 173
DB 121 GGSQGGSGGGSGGSGGSDTLTQSPSPVVIPEGESVISCSSKSLIYSDGSDYLFVFLQRP 180
QY 174 KAPKLIVDVSNRPISGNRFSKSGDTPASLTISGLQAEADYVCSFANSGLPFGG 233
DB 181 QSPQLLIYRMSNLASGVDPFRFGSGGTSTFLIRISREAVDGVYVYCHREYPLTETAG 240
QY 234 TKV 236
DB 241 TKL 243

RESULT 3
S70442
Ig heavy chain precursor V region (mu) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000
C:Accession: S70442
R:Cuissinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelie, C.
Mol. Immunol. 29, 1363-1373, 1992
A:Title: IGM kappa/lambda BBV human B cell clone: an early step of differentiation of f
A:Reference number: S70442; MUID:93024508; PMID:1383695
A:Accession: S70442
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-140 <CUI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 44.0%; Score 549.5; DB 2; Length 140;
Best Local Similarity 87.6%; Pred. No. 1.8e-31;
Matches 106; Conservative 3; Mismatches 7; Indels 5; Gaps 1;
QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSYSSMSWVRQAPGKLEWVAVISYDGSNKYY 60
DB 20 QVQLVESGGGVQPGGSLRLSCAASGFTFSNFMHWVRQAPGKLEWVAFIRYDGSNKYY 79
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARDR-----YFDLWGRGTLTVSS 115
DB 80 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARDHIVGATYFDYWGQGTTLTVSS 139
QY 116 G 116
DB 140 G 140

RESULT 4
F36005
Ig heavy chain V region (M49) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C:Accession: F36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: F36005
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SCH>
A:Cross-references: GB:M34026
C:Genetics:
A:Gene: GDB:IGH@; IGHDI1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 43.8%; Score 547; DB 2; Length 119;
Best Local Similarity 89.1%; Pred. No. 2.2e-31;
Matches 106; Conservative 5; Mismatches 4; Indels 4; Gaps 1;
QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSYSSMSWVRQAPGKLEWVAVISYDGSNKYY 60
DB 1 QVQLVESGGGVQPGGSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARDR---YFDLWGRGTLTVSS 115
DB 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARDKASDAFDYWGQGTTLTVSS 119

RESULT 5
G36005
Ig heavy chain V region (M74) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C:Accession: G36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: G36005
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-121 <SCH>
A:Cross-references: GB:M34031
C:Genetics:
A:Gene: GDB:IGH@; IGHDI1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 43.7%; Score 546; DB 2; Length 121;
Best Local Similarity 88.4%; Pred. No. 2.7e-31;
Matches 107; Conservative 3; Mismatches 5; Indels 6; Gaps 1;
QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSYSSMSWVRQAPGKLEWVAVISYDGSNKYY 60
DB 1 QVQLVESGGGVQPGGSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARDR-----YFDLWGRGTLTVSS 114
DB 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARDKQWALFDYWGQGTTLTVSS 120
QY 115 S 115
DB 121 S 121

RESULT 6
S31603
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

Accession: S31603
Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
Submitted to the EMBL Data Library, June 1992
Description: Mechanisms that generate human immunoglobulin diversity operate from the
Reference number: S31585
Accession: S31603
Status: preliminary
Molecule type: mRNA
Residues: 1-132 <CUI>
Cross-references: EMBL:Z14168; NID:g30999; PIDN:CAA78537.1; PID:g31000
Superfamily: immunoglobulin V region; immunoglobulin homology
Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 43.3%; Score 541; DB 2; Length 132;
Best Local Similarity 89.7%; Pred. No. 6.5e-31;
Matches 105; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

2Y 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKLEWVAIVSYDGSNKYY 60
16 QVQLVESGGGVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKLEWVAIVSYDGSNKYY 75
2Y 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVVYCARD--RYFDLWGRGTLTVVSS 115
2b 76 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVVYCARDLFYFDYNGQGLTVTVSS 132

RESULT 7
JC5322
p53 specific single-chain antibody Pab421 - human
Species: Homo sapiens (man)
Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
Accession: JC5322
Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
Reference number: JC5322; MUID:97168950; PMID:9016757
Accession: JC5322
Molecule type: mRNA
Residues: 1-233 <JAN>
Experimental source: hybridoma cell
Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 43.2%; Score 540.5; DB 2; Length 233;
Best Local Similarity 49.2%; Pred. No. 1.3e-30;
Matches 116; Conservative 31; Mismatches 84; Indels 5; Gaps 4;

QY 5 QESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKLEWVAIVSYDGSNKYYADSV 64
Db 1 QESGAELVRSASVSLCTTSFNFINDYHFWKXKPEQGLEWIGRIDPENGADWTRSS 60
QY 65 KGRFTISRDNKNTLYLQMSLRAEDTAVVYCARDYFDLWGRGTLTVVSSGGGGGGGG 124
Db 61 GVKATWADTSTNTAYLQSLTSDTAVVYC--NAGMDYWGQGTITVTVSSGGGGGGGGA 118
QY 125 SGGGGSQALTO-PASVSGSPQQTITISCTQSS-DICAVNVSVWYQYQPKAPKLLIYD 182
Db 119 SGGGGSDIELTQSPASLAVSLQQRATISCRASKSVSTSGYSMEWNCQKPGPPRLIYL 178
QY 183 VSNRSGISNRPSSGSGDTSALTSIGLQADEADYVCSFANSGLPFGGKTUTV 238
Db 179 VSNLSEGVPAPESSGSGDFTLNHPVEESDAATYVQCQHIREL-TRSEGGTKLEI 233

RESULT 8
E36005
Ig heavy chain V region (W72) - human
Species: Homo sapiens (man)
Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
Accession: E36005
R Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene

Reference number: A36005; MUID:90349571; PMID:2117273
Accession: E36005
Status: preliminary
Molecule type: mRNA
Residues: 1-122 <SCH>
Cross-references: GB:M34030
Genetics:
C.Gens: GDB:IGH0; IGHDY1
Cross-references: GDB:118731; OMIM:146910
Map position: 14q32.33-14q32.33
Superfamily: immunoglobulin V region; immunoglobulin homology
Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 43.2%; Score 539.5; DB 2; Length 122;
Best Local Similarity 85.1%; Pred. No. 7.6e-31;
Matches 105; Conservative 5; Mismatches 5; Indels 7; Gaps 1;

QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 1 QVQLVESGGGVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKLEWVAIVSYDGSNKYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVVYCARDY-----FDLWGRGTLTVV 113
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVVYCARDHSSSSWYGMVWGQGTITTV 120
QY 114 SS 115
Db 121 SS 122

RESULT 9
S31679
Ig heavy chain V region - human (fragment)
Species: Homo sapiens (man)
Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
Accession: S31679
Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
Submitted to the EMBL Data Library, June 1992
Description: Mechanisms that generate human immunoglobulin diversity operate from the
Reference number: S31585
Accession: S31679
Status: preliminary
Molecule type: mRNA
Residues: 1-134 <CUI>
Cross-references: EMBL:Z14203; NID:g30965; PIDN:CAA78572.1; PID:g30966
Superfamily: immunoglobulin V region; immunoglobulin homology
Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 43.1%; Score 539; DB 2; Length 134;
Best Local Similarity 90.4%; Pred. No. 9e-31;
Matches 104; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 20 QVQLVESGGGVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKLEWVAIVSYDGSNKYY 79
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVVYCARDYFDLWGRGTLTVVSS 115
Db 80 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVVYCARDHSSSGDYWGQGTITTVVSS 134

RESULT 10
S38493
Ig heavy chain - human (fragment)
Species: Homo sapiens (man)
Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
Accession: S38493
R.Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.
Submitted to the EMBL Data Library, June 1993
Description: Human antibody fragments specific for human blood group antigens from a p
Reference number: S38488

A:Accession: S38493
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-123 <MAR>
A:Cross-references: EMBL:Z23036; NID:G414033; PIDN:CAA80571.1; PID:G414034
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 43.0%; Score 538; DB 2; Length 123;
Best Local Similarity 85.4%; Pred. No. 9.7e-31;
Matches 105; Conservative 4; Mismatches 6; Indels 8; Gaps 1;

QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKLEWAVISYDGSNKYY 60
DB 1 QVQLQESGGGVQPGGSLRLSCAASGFTFSSYAMHWVRQAPGKLEWAVISYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARD-----YFDLWGRGTLVTT 112
DB 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARDRAESNNWYVYMDVWGKGTVT 120

QY 113 VSS 115
DB 121 VSS 123

RESULT 11
S46391
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46391
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 48-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <FIG>
A:Cross-references: EMBL:Z31687; NID:G509784; PIDN:CAA83492.1; PID:G1335144
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 43.0%; Score 537.5; DB 2; Length 114;
Best Local Similarity 90.4%; Pred. No. 9.7e-31;
Matches 104; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKLEWAVISYDGSNKYY 60
DB 1 QVNLRESGGGLVQPGGSLRLSCASGFTFSSYAMHWVRQAPGKLEWAVISYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARDYFDLWGRGTLVTTSS 115
DB 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARD-FGDYWGQGTLLTVSS 114

RESULT 12
S46390
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46390
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <FIG>
A:Cross-references: EMBL:Z31686; NID:G509782; PIDN:CAA83491.1; PID:G1335143

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 42.8%; Score 534.5; DB 2; Length 114;
Best Local Similarity 90.4%; Pred. No. 1.6e-30;
Matches 104; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKLEWAVISYDGSNKYY 60
DB 1 EVQLVESGGGVQPGGSLRLSCAASGFTFSSYAMHWVRQAPGKLEWAVISYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARDYFDLWGRGTLVTTSS 115
DB 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARD-WGDYWGQGTLLTVSS 114

RESULT 13
S31116
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31116
R:Raaphorst, F.M.; Timmers, B.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurma
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31116
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-118 <RAA>
A:Cross-references: EMBL:X62966
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 42.8%; Score 534.5; DB 2; Length 118;
Best Local Similarity 88.1%; Pred. No. 1.6e-30;
Matches 104; Conservative 4; Mismatches 7; Indels 3; Gaps 1;

QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKLEWAVISYDGSNKYY 60
DB 1 QVQLVESGGGVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKLEWAVISYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCARD--RYFDLWGRGTLVTTSS 115
DB 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCATDGGKAAFDWGGTWTVSS 118

RESULT 14
S31117
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31117
R:Raaphorst, F.M.; Timmers, B.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurma
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31117
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-122 <RAA>
A:Cross-references: EMBL:X62967
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 42.8%; Score 534.5; DB 2; Length 122;
Best Local Similarity 86.1%; Pred. No. 1.7e-30;
Matches 105; Conservative 3; Mismatches 7; Indels 7; Gaps 1;

QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSYSSMSWVROAPGKLEWVAIVSYDGSNKYY 60
DB 1 QVQLVESGGGVQPGGSLRLSCAASGFTFSYSGHWRQAPGKLEWVAIVTYDGSNKYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYYCARD-----RYFDLWGRGTLTV 113
DB 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYYCARDFFAPPENWSHFDYWGQGLTV 120
QY 114 SS 115
DB 121 SS 122

RESULT 15

PH1645
Ig heavy chain V region (clone 6C8) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C/Accession: PH1645
R/Hillson, J.L.; Karr, N.S.; Oppiger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A/Reference number: PH1645; MUID:93301610; PMID:8315388
A/Accession: PH1645
A/Molecule type: mRNA
A/Residues: 1-111 <HIL>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/7-90/Domain: immunoglobulin homology <IMV>

Query Match 42.6%; Score 533; DB 2; Length 111;
Best Local Similarity 92.8%; Pred. No. 1.9e-30;
Matches 103; Conservative 2; Mismatches 2; Indels 4; Gaps 1;
QY 9 GGLVQPGGSLRLSCAASGFTFSYSSMSWVROAPGKLEWVAIVSYDGSNKYYADSVKGRF 68
DB 1 GGVQPGGSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAIVSYDGSNKYYADSVKGRF 60
QY 69 TISRDNKNTLYLQNSLRAEDTAVYYCARD-----YFDLWGRGTLTVSS 115
DB 61 TISRDNKNTLYLQNSLRAEDTAVYYCARDRGAWYFDLWGRGTLTVSS 111

Search completed: March 15, 2004, 07:28:22
Job time : 21 secs

GenCore version 5.1.6
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M protein - protein search, using sw model

run on: March 15, 2004, 07:26:28 ; Search time 406 Seconds
(without alignments)
124,300 Million cell updates/sec

title: US-09-620-955B-6

effect score: 1250

sequence: 1 QVQLQESGGGVLPQGGSLRL.....CSSFANSGPLFGGCTKVTVL 239

scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 809742 seqs, 211153259 residues

total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/FCI_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/FCIUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1110	88.8	254	10	US-09-880-748-983
2	1106	88.5	256	10	US-09-880-748-839
3	1097	87.8	252	10	US-09-880-748-1627
4	1096	87.7	254	10	US-09-880-748-981
5	1095.5	87.6	241	10	US-09-880-748-2055
6	1093	87.4	252	10	US-09-880-748-956
7	1089.5	87.2	251	10	US-09-880-748-955
8	1089.5	87.2	251	10	US-09-880-748-1317
9	1088.5	87.1	251	10	US-09-880-748-1114
10	1084.5	86.8	253	10	US-09-880-748-1003
11	1082.5	86.6	251	10	US-09-880-748-1332
12	1079	86.3	254	10	US-09-880-748-1701
13	1079	86.3	254	10	US-09-880-748-1759
14	1078	86.2	256	10	US-09-880-748-1332
15	1077.5	86.2	253	10	US-09-880-748-989

16	1077	86.2	254	10	US-09-880-748-881	Sequence 881, App
17	1073.5	85.9	253	10	US-09-880-748-1007	Sequence 1007, App
18	1072	85.8	244	10	US-09-880-748-1910	Sequence 1910, App
19	1067	85.4	234	10	US-09-880-748-977	Sequence 977, App
20	1065	85.2	240	10	US-09-880-748-2047	Sequence 2047, App
21	1065	85.2	254	10	US-09-880-748-1428	Sequence 1428, App
22	1064.5	85.2	253	10	US-09-880-748-1449	Sequence 1449, App
23	1063	85.0	254	10	US-09-880-748-1075	Sequence 1075, App
24	1062	85.0	254	10	US-09-880-748-1735	Sequence 1735, App
25	1061.5	84.9	251	10	US-09-880-748-1605	Sequence 1605, App
26	1061.5	84.9	253	10	US-09-880-748-1337	Sequence 1337, App
27	1061	84.9	246	10	US-09-880-748-1314	Sequence 1314, App
28	1061	84.9	254	10	US-09-880-748-1673	Sequence 1673, App
29	1058	84.6	240	10	US-09-880-748-1898	Sequence 1898, App
30	1057	84.6	252	10	US-09-880-748-1431	Sequence 1431, App
31	1056.5	84.5	247	10	US-09-880-748-915	Sequence 915, App
32	1056	84.5	252	10	US-09-880-748-1690	Sequence 1690, App
33	1055	84.4	240	10	US-09-880-748-1930	Sequence 1930, App
34	1055	84.4	246	10	US-09-880-748-1324	Sequence 1324, App
35	1055	84.4	250	10	US-09-880-748-883	Sequence 883, App
36	1053	84.2	246	10	US-09-880-748-2077	Sequence 2077, App
37	1052.5	84.2	243	10	US-09-880-748-995	Sequence 995, App
38	1052	84.2	252	10	US-09-880-748-1634	Sequence 1634, App
39	1051	84.1	248	10	US-09-880-748-1782	Sequence 1782, App
40	1050.5	84.0	247	14	US-10-322-673-48	Sequence 48, Appl
41	1050.5	84.0	247	14	US-10-322-673-48	Sequence 1653, App
42	1050	84.0	248	10	US-09-880-748-1653	Sequence 925, App
43	1049.5	84.0	251	10	US-09-880-748-925	Sequence 1819, App
44	1045.5	83.6	255	10	US-09-880-748-1819	Sequence 1404, App
45	1045	83.6	248	10	US-09-880-748-1404	

ALIGNMENTS

RESULT 1
US-09-880-748-983
; Sequence 983, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR FILING DATE: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 60/293,499
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 983
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-983

Query Match 88.8%; Score 1110; DB 10; Length 254;
Best Local Similarity 84.2%; Pred. No. 7.1e-73;
Matches 213; Conservative 14; Mismatches 12; Indels 14; Gaps 2;

QY 1 QVQLQESGGGVLPQGGSLRLCAASGFTFSYMSVQRQAPGKLEWVAVISYDGSNKYY 60
Db 1 QVQLQESGGGVLPQGGSLRLCAASGFTFSYMSVQRQAPGKLEWVAVISYDGSNKYY 60
QY 61 ADVKRGRTISRDNSKNTLYIQMSLRAEDTAVYYCARDR-----YFDLWGR 107
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Db		61	ADSVKGRFTSRDNRKNTLYLQNNLSRAEDATVYCARBEGFVDILTYGGYGGYFYWGK	120
QY		108	GTLVTVSSGGGGSGGGSGGGGSQSALTPASVSGSPGQSITISCTGTSSDITGANNYSW	167
Db		121	GTMTVSSGGGGSGGGSGGGGSQSVLTPASVSGSPGQSITISCTGTSSDVGGSYYSW	180
QY		168	YQQYPGKAPKLLIYDVNRPSGISNRFSGSKGDTASLTISGLQADEADYVCSF-ANS	226
Db		181	YQQHPPGKAPKLMITYEGKRPSGVSNRFPSGSKGNTASLTISGLQADEADYVCSYITRS	240
QY		227	GFLEGGGTKTVL	239
Db		241	TRVFGGGTKTLV	253

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RESULT 2
US-09-880-748-839
; Sequence 839, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PPS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 839
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-839

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Query Match	88.5%;	Score	1106;	DB	10;	Length	256;
Best Local Similarity	83.9%;	Pred. No.	1.4e-72;				
Matches	213;	Conservative	12;	Mismatches	13;	Indels	15;
Gaps	2;						
2	QVQESGGGLVQPGGSLRLSCAASGFTFSSYSMWVRQAPGKLEWVAIVSYDGSNKYYA	61					
2	VQLVQSGGGVLPQGSLELSCAASGFTFSSYGMHWVRQAPGKLEWVAIVSYDGSNKYYA	61					
62	DSVKGRTTISDNSKNTLYLQMSLRADETAVYICADR-----YFDLWG	106					
62	DSVKGRTTISDNSKNTLYLQMSLRADETAVYICADREAYVDILTGYLYYYNDVWG	121					
107	RGTLVTVSSGGGSGGGSGGGGSSQSLTQPSVSGSPGQSIITISCTGTSSDIGAYNTVS	166					
122	RGTTVTVSSGGGSGGGSGGGGSSQSLTQPSVSGSPGQSIITISCTGTSSDVGGVNTVS	181					
167	WYQYPGKAPKLLIYDYNPSGTSNEPFGSKSGDTSALTISGLQAEADYVCSGF-AN	225					
182	WYQHPGKAPKMLIYEGSKRFPVSGVNRFGSKSGNTASLTISGLQAEADYVCSYTTG	241					
226	SGPLFGGKTVTL	239					
242	STRVFGGKTVL	255					

RESULT 3
US-09-880-748-1627
; Sequence 1627, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:

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; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Buys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1627
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-1627

Query Match      87.8%; Score 1097; DB 10; Length 252;
Best Local Similarity 84.58; Pred. No. 6.1e-72;
Matches 212; Conservative 12; Mismatches 15; Indels 12; Gaps 2;

QY      1  QVQLQESGGGLVPGGSLRLSCAASGFTTSSYMSWRQAPGKGLEWVAIVSYDGSNKYY 60
Db      1  QVQLVQSGGGVQPGSLRLSCAASGFTTSSYGMHWRAQPGKLEWVAIVSYDGSNKYY 60

QY      61  ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARD-----RYFDLWGRGT 109
Db      61  ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARSPGDDILTYVKKYFYDWGGQT 120

QY      110  LVTVSSGGGGSGGGSGGGGQSALTPQASVSGSPGQSITTSCTGTSDDIGAYNVSVWYQ 169
Db      121  LVTVSSGGGGSGGGSGGGGQSQVLTPQASVSGSPGQSITTSCTGTSDDVGVGYNVSVWYQ 180

QY      170  QYPKAPKLLIYDVSNRPSCIINRFGSGSGGTASLITSGLOAREADYVCSGF-ANSGP 228
Db      181  QHPKAPKPLMIYSGKKRPQSGVSNRFGSGSGMTASLTSGLOAREADYVCSGYTTRSTR 240

QY      229  LFGGGTKVTVL 239
Db      241  VFGGGTKLTVL 251

```

RESULT 4
US-09-880-748-991
Sequence 981, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3439
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 981
LENGTH: 254
TYPE: PRT

PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 955
LENGTH: 251
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-955

Query Match 87.2%; Score 1089.5; DB 10; Length 251;
Best Local Similarity 83.6%; Pred. No. 2.1e-71;
Matches 209; Conservative 14; Mismatches 16; Indels 11; Gaps 2;

QY 1 QVQLQESGGGLVQPGGSLRLCSAASGFTFSYSSMSWVRQAPGKLEWVAIVSYDGSNKYY 60
DB 1 EVQLVESGGGVQPVGRSRLCSAASGFTFSYSGHWRQAPGKLEWVAIVSYDGSNKYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARSHYDILTLGLNYYFDLWGRGTL 110
DB 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARSHYDILTLGLNYYFDLWGRGTM 120
QY 111 VTVSSGGGGSGGGSGGGSGGSSQSLTQPASVSGSPGQITISCTGSSDIDGAYNVVSWYQQ 170
DB 121 VTVSSGGGGSGGGSGGGSGGSSQSLTQPASVSGSPGQITISCTGSSDIDGAYNVVSWYQQ 180
QY 171 YPGKAPKLLIYDVSNRPSGISNRPSKSGSDTASLTISGLQAEDEADYYCSSF-ANSGPL 229
DB 181 HPGKAPKLLIYEGSKRPSGVNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTTTRSTRV 240
QY 230 FGGGTKVTVL 239
DB 241 FGGGTKLTVL 250

RESULT 8

US-09-880-748-1317
Sequence 1317, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:

APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: P2523
CURRENT APPLICATION NUMBER: US/09/880,748

PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 1317
LENGTH: 251
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1317

Query Match 87.2%; Score 1089.5; DB 10; Length 251;
Best Local Similarity 83.6%; Pred. No. 2.1e-71;
Matches 209; Conservative 14; Mismatches 16; Indels 11; Gaps 2;

QY 1 QVQLQESGGGLVQPGGSLRLCSAASGFTFSYSSMSWVRQAPGKLEWVAIVSYDGSNKYY 60
DB 1 QITLKGSGGVVQPVGRSRLCSAASGFTFSYSGHWRQAPGKLEWVAIVSYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARSHYDILTLGLNYYFDLWGRGTL 110
DB 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARSHYDILTLGLNYYFDLWGRGTL 120
QY 111 VTVSSGGGGSGGGSGGGSGGSSQSLTQPASVSGSPGQITISCTGSSDIDGAYNVVSWYQQ 170
DB 121 VTVSSGGGGSGGGSGGGSGGSSQSLTQPASVSGSPGQITISCTGSSDIDGAYNVVSWYQQ 180
QY 171 YPGKAPKLLIYDVSNRPSGISNRPSKSGSDTASLTISGLQAEDEADYYCSSF-ANSGPL 229
DB 181 HPGKAPKLLIYEGSKRPSGVNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTTTRSTRV 240
QY 230 FGGGTKVTVL 239
DB 241 FGGGTKLTVL 250

RESULT 9

US-09-880-748-1114
Sequence 1114, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:

APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: P2523
CURRENT APPLICATION NUMBER: US/09/880,748

PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 1114
LENGTH: 251
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1114

Query Match 87.1%; Score 1088.5; DB 10; Length 251;
Best Local Similarity 83.2%; Pred. No. 2.5e-71;
Matches 208; Conservative 16; Mismatches 15; Indels 11; Gaps 2;

QY 1 QVQLQESGGGLVQPGGSLRLCSAASGFTFSYSSMSWVRQAPGKLEWVAIVSYDGSNKYY 60
DB 1 EVQLVESGGGVQPVGRSRLCSAASGFTVNSYAMHWVRQAPGKLEWVAIVSYDGSNKYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARSHYDILTLGLNYYFDLWGRGTL 110
DB 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARSHYDILTLGLNYYFDLWGRGTT 120
QY 111 VTVSSGGGGSGGGSGGGSGGSSQSLTQPASVSGSPGQITISCTGSSDIDGAYNVVSWYQQ 170
DB 121 VTVSSGGGGSGGGSGGGSGGSSQSLTQPASVSGSPGQITISCTGSSDIDGAYNVVSWYQQ 180
QY 171 YPGKAPKLLIYDVSNRPSGISNRPSKSGSDTASLTISGLQAEDEADYYCSSF-ANSGPL 229
DB 181 HPGKAPKLLIYEGSKRPSGVNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTTTRSTRV 240
QY 230 FGGGTKVTVL 239
DB 241 FGGGTKLTVL 250

RESULT 10

US-09-880-748-1003
Sequence 1003, Application US/09880748

Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
FILE REFERENCE: PFS23
CURRENT APPLICATION NUMBER: US/09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1003
LENGTH: 253
TYPE: PRT
ORGANISM: Homo sapiens
IS-09-880-748-1003

Query Match 86.8%; Score 1084.5; DB 10; Length 253;
Best Local Similarity 82.9%; Pred. No. 4.9e-71;
Matches 209; Conservative 14; Mismatches 16; Indels 13; Gaps 2;

2Y 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKGLWVAIVSYDGSNKYY 60
2b 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKGLWVAIVSYDGSNKYY 60

2Y 61 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYVCARDRYFDL-----WGRG 108
2b 61 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYVCARDRYFDL-----WGRG 108

2Y 109 TLVTVSSGGGGGGGGGGGGSGQSALTQTPASVSGSPGQSITISCTGTSSDYGAINVYSWY 168
2b 121 TLVTVSSGGGGGGGGGGGGSGQSALTQTPASVSGSPGQSITISCTGTSSDYGAINVYSWY 180

2Y 169 QYPGKAPKLLIYDVSNRPSGISNRFSGSKGSDTASLTISGLQAEADYVCSF-ANSG 227
2b 181 QHPGKAPKLLIYDVSNRPSGISNRFSGSKGSDTASLTISGLQAEADYVCSF-ANSG 240

2Y 228 PLFGGGTKVTVL 239
2b 241 RVFGGGTKLTVL 252

RESULT 11
US-09-880-748-1332
; Sequence 1332, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1332

; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1332

Query Match 85.6%; Score 1082.5; DB 10; Length 251;
Best Local Similarity 83.2%; Pred. No. 6.8e-71;
Matches 208; Conservative 14; Mismatches 17; Indels 11; Gaps 2;

QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKGLWVAIVSYDGSNKYY 60
Db 1 EVQLVQSGGGVQVQPGRLSLRLSCAASGFTFSSYSMSWVRQAPGKGLWVAIVSYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYVCARDRYFDL-----YDLMGRGTL 110
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYVCARDRYFDL-----YDLMGRGTL 120

QY 111 VTSSGGGGGGGGGGGGSGQSALTQTPASVSGSPGQSITISCTGTSSDYGAINVYSWY 170
Db 121 VTSSGGGGGGGGGGGGSGQSALTQTPASVSGSPGQSITISCTGTSSDYGAINVYSWY 180

QY 171 YPGKAPKLLIYDVSNRPSGISNRFSGSKGSDTASLTISGLQAEADYVCSF-ANSGPL 229
Db 181 HPGKAPKLLIYDVSNRPSGISNRFSGSKGSDTASLTISGLQAEADYVCSF-ANSGPL 240

QY 230 FGGGTKVTVL 239
Db 241 FGGGTKLTVL 250

RESULT 12
US-09-880-748-1701
; Sequence 1701, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1701
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1701

Query Match 86.3%; Score 1079; DB 10; Length 254;
Best Local Similarity 81.8%; Pred. No. 1.2e-70;
Matches 207; Conservative 18; Mismatches 14; Indels 14; Gaps 2;

QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKGLWVAIVSYDGSNKYY 60
Db 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKGLWVAIVSYDGSNKYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYVCARDRYFDL-----DLNWR 107
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYVCARDRYFDL-----DLNWR 120

QY 108 GTLVTVSSGGGGGGGGGGGGSGQSALTQTPASVSGSPGQSITISCTGTSSDYGAINVYSW 167
Db 121 GTLVTVSSGGGGGGGGGGGGSGQSALTQTPASVSGSPGQSITISCTGTSSDYGAINVYSW 180

QY 168 YQYFGKAPKLLIYDVSNRPSGINSRFGSGKSGDTASLTISGLQAEADYDCCSF-ANS 226
 Db 181 YQYFGKAPKLLIYDVSNRPSGINSRFGSGKSGNTASLTISGLQAEADYDCCSYTTS 240
 QY 227 GFLFGGKTKTVL 239
 Db 241 TRVFGGKTKTVL 253

RESULT 13
 US-09-880-748-1759
 ; Sequence 1759, Application US/09880748
 ; Publication No. US2003005937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1759
 ; LENGTH: 254
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-880-748-1759

Query Match 86.3%; Score 1079; DB 10; Length 254;
 Best Local Similarity 82.2%; Pred. No. 1.2e-70;
 Matches 208; Conservative 16; Mismatches 15; Indels 14; Gaps 2;

QY 1 QVLOESGGGLVQPGGSLRLSCAASGFTFSYSGMSWVRQAPGKLEWVAIVSYDGSNKYY 60
 Db 1 QVQLVQSGGVLVQPGGSLRLSCAASGFTFSYGHVWRQAPGKLEWVAIVSYDGSIRKY 60
 QY 61 ADSVGRFTISRDNKNTLYLQMSLRAEDTAVYICAREGSDYLTGYVGVGRMDVWGR 120
 Db 61 ADSVGRFTISRDNKNTLYLQMSLRAEDTAVYICAREGSDYLTGYVGVGRMDVWGR 120
 QY 108 GTLVTVSSGGGGGGGGGGGSGQSALTQPASVSGSPGQITISCTGTSSDYGAYNVSW 167
 Db 121 GTMTVSSGGGGGGGGGGGSGQSALTQPASVSGSPGQITISCTGTSSDVGGINVSW 180
 QY 168 YQYFGKAPKLLIYDVSNRPSGINSRFGSGKSGDTASLTISGLQAEADYDCCSF-ANS 226
 Db 181 YQYFGKAPKLLIYDVSNRPSGINSRFGSGKSGNTASLTISGLQAEADYDCCSYTTS 240
 QY 227 GFLFGGKTKTVL 239
 Db 241 TRVFGGKTKTVL 253

RESULT 14
 US-09-880-748-1392
 ; Sequence 1392, Application US/09880748
 ; Publication No. US2003005937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15

Query Match 86.3%; Score 1079; DB 10; Length 254;
 Best Local Similarity 82.2%; Pred. No. 1.2e-70;
 Matches 208; Conservative 16; Mismatches 15; Indels 14; Gaps 2;

QY 1 QVLOESGGGLVQPGGSLRLSCAASGFTFSYSGMSWVRQAPGKLEWVAIVSYDGSNKYY 60
 Db 1 QVQLVQSGGVLVQPGGSLRLSCAASGFTFSYGHVWRQAPGKLEWVAIVSYDGSIRKY 60
 QY 61 ADSVGRFTISRDNKNTLYLQMSLRAEDTAVYICAREGSDYLTGYVGVGRMDVWGR 120
 Db 61 ADSVGRFTISRDNKNTLYLQMSLRAEDTAVYICAREGSDYLTGYVGVGRMDVWGR 120
 QY 108 GTLVTVSSGGGGGGGGGGGSGQSALTQPASVSGSPGQITISCTGTSSDYGAYNVSW 167
 Db 121 GTMTVSSGGGGGGGGGGGSGQSALTQPASVSGSPGQITISCTGTSSDVGGINVSW 180
 QY 168 YQYFGKAPKLLIYDVSNRPSGINSRFGSGKSGDTASLTISGLQAEADYDCCSF-ANS 226
 Db 181 YQYFGKAPKLLIYDVSNRPSGINSRFGSGKSGNTASLTISGLQAEADYDCCSYTTS 240
 QY 227 GFLFGGKTKTVL 239
 Db 241 TRVFGGKTKTVL 253

RESULT 14
 US-09-880-748-1392
 ; Sequence 1392, Application US/09880748
 ; Publication No. US2003005937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15

Query Match 86.2%; Score 1077.5; DB 10; Length 253;
 Best Local Similarity 83.3%; Pred. No. 1.6e-70;

QY 1 QVLOESGGGLVQPGGSLRLSCAASGFTFSYSGMSWVRQAPGKLEWVAIVSYDGSNKYY 60
 Db 1 QVQLVQSGGVLVQPGGSLRLSCAASGFTFSNDMSWVRQAPGKLEWVSGISGSGSKYY 60
 QY 61 ADSVGRFTISRDNKNTLYLQMSLRAEDTAVYICARDRY-----FDLW 105
 Db 61 ADSVGRFTISRDNKNTLYLQMSLRAEDTAVYICARDRYDILTGYVIGLDDAFDIW 120
 QY 106 GRGTLTVSSGGGGGGGGGGGSGQSALTQPASVSGSPGQITISCTGTSSDYGAYNV 165
 Db 121 QGTLTVTVSSGGGGGGGGGGGSGQSALTQPASVSGSPGQITISCTGTSSDVGGINV 180
 QY 166 SWYQVPGKAPKLLIYDVSNRPSGINSRFGSGKSGDTASLTISGLQAEADYDCCSF-A 224
 Db 181 SWYQVPGKAPKLLIYDVSNRPSGINSRFGSGKSGNTASLTISGLQAEADYDCCSYTT 240
 QY 225 NSGFLFGGKTKTVL 239
 Db 241 RSTRVFGGKTKTVL 255

RESULT 15
 US-09-880-748-989
 ; Sequence 989, Application US/09880748
 ; Publication No. US2003005937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 989
 ; LENGTH: 253
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-880-748-989

Query Match 86.2%; Score 1077.5; DB 10; Length 253;
 Best Local Similarity 83.3%; Pred. No. 1.6e-70;

Matches 210;		Conservative	14;	Mismatches	15;	Indels	13;	Gaps	3;
Y	1	QVQLAESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKGLWYAVISYDGSNKYY	60						
b	1	QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLWYAVISYDGSNKYY	60						
Y	61	ADSVKGRFTISRDNKNTLYLQWNSLRPEDTAVYICARDR-----YF---DLWGRG	108						
b	61	ADSVKGRFTISRDNKNTLYLQWNSLRPEDTAVYICARDR-----YF---DLWGRG	120						
Y	109	TLVTSSGGGGGGGGGGGSGQSALTQPASVSGSGQSITISCTGSDIGAYNVVSWY	168						
b	121	TLVTSSGGGGGGGGGGGSGQSALTQPASVSGSGQSITISCTGSDIGAYNVVSWY	180						
Y	169	QQYPGKAPKLLIYDVSNRPISGNSRPSGSKSGDTASLTISGLQAEDEADYYCSSF-ANSG	227						
b	181	QQHPGKAPKLLIYDVSNRPISGNSRPSGSKSGDTASLTISGLQAEDEADYYCSSYTRST	240						
Y	228	PLFGGTTKVTVL	239						
b	241	RVFGGTTKVTVL	252						

Search completed: March 15, 2004, 07:36:34
Job time : 407 secs

Db 40 QVQLQSGGGLVPGGSLKLSAASGDSFERYNWSVRQAPGKGLWIGINPDSSTINY 99
 QY 61 ADSVKGRFTISRDNSKNTLYIQMNSLRADTAIVYCARDFD---LWGRGLTVTVSSGG 117
 Db 100 TFLSKDKFTIISRDNAKNTLYIQMNSLRADTAIVYCARDFD---LWGRGLTVTVSSGG 159
 QY 118 GSGGGGGGGGSGGSSALFQ-PASVSGSGGSGITISCTGSDIGAVNYVSWYQYFGKAP 176
 Db 160 GSGGGGGGGGSGGSDIELTQSPASLSASVGVNTITCRASGN---IHNLYAWYQKQKSP 216
 QY 177 KLLIYDVNRRPSGISNRFSGSKGSDTASLTISGLQAEDEADYVCSFANSGLFPGGKTV 236
 Db 217 QLLVYNKTLADGVPFRSGSGTQISLKLNSLPEDFGSYVQGHFWITPTFGGGLK 276
 QY 237 TV 238
 Db 277 EI 278

RESULT 2

Q921A6 PRELIMINARY; PRT; 241 AA.
 AC Q921A6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Anti-CBA 79 single chain Fv fragment (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98170165; PubMed=9509426;
 RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
 RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
 RT "Cloning and characterization of cDNAs encoding VH and VL of a
 RT monoclonal anti-CBA antibody (CEA 79) cross-reactive with NCA-95 and
 RT generation of a single-chain Fv molecule (scFv).";
 RL Mol. Cells 7:816-819 (1997).
 DR EMBL; U88067; AAB48044.1; -.
 DR InterPro; IPR007110; IG-Like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_2.
 DR SMART; SM00406; IGV_2.
 DR PROSITE; PS50835; IG_LIKE; 2.
 FT NON_TER 1 241
 FT NON_TER 241 241
 SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 49.7%; Score 621; DB 11; Length 241;
 Best Local Similarity 53.7%; Pred. No. 6.6e-41;
 Matches 131; Conservative 33; Mismatches 64; Indels 16; Gaps 7;

QY 1 QVQLQSGGGLVPGGSLRLSCAASGFTFSYSSMSWRQAPGKGLWVAIVSYDGNKY 60
 Db 1 QVQLQSGGGLVPGGSLRLSCAASGFTFSYSSMSWRQAPGKGLWVAIVSYDGNKY 60
 QY 61 ADSVKGRFTISRDNSKNTLYIQMNSLRADTAIVYCARDFD---RYFDLWGRGLTVTVSSGG 117
 Db 61 ADDFKRFAFSLTASASTAYLIQNNLNKEDTATVFCARKDLLRYFDYWGQTTTVTVSSGG 120
 QY 118 GSGGGGGGGGSGGSSALFQ-PASVSGSGGSGITISCTGSDIGAVNYVSWYQYFGKAP 176
 Db 121 GSGGGGGGGGSGGSDIELTQSPSSLSASVGVNTITCK-ASQDN--KYAWYQKQKSP 177
 QY 177 K---LLIYDVNRRPSGISNRFSGSKGSDTASLTISGLQAEDEADYVCSFANSGLFPGG 232
 Db 178 RGAHTLHIY----IQGIPSRFSGSGGRDYSFISNLEPDIATYICLHYDNL-HTFGG 232
 QY 233 GTKV 236
 Db 233 GTKL 236

RESULT 3

Q7TQM2 PRELIMINARY; PRT; 243 AA.
 AC Q7TQM2;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE scFv 6H8 protein (Fragment).
 GN SCFV 6H8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Balb/C;
 RA Peter J.C., Eftekhari P., Billiald P., Wallukat G.;
 RT "scFv single chain antibody variable fragment as inverse agonist for
 RT the beta-2 adrenergic receptor";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ574851; CAB00495.1; -.
 FT NON_TER 1 243
 SQ SEQUENCE 243 AA; 25976 MW; BEFF64D2DCF4F76 CRC64;

Query Match 48.0%; Score 600; DB 11; Length 243;
 Best Local Similarity 52.3%; Pred. No. 2.9e-39;
 Matches 126; Conservative 40; Mismatches 67; Indels 8; Gaps 7;

QY 1 QVQLQSGGGLVPGGSLRLSCAASGFTFSYSSMSWRQAPGKGLWVAIVSYDGN-KY 59
 Db 1 QVQLQSGGGLVPGGSLRLSCAASGFTFSYSSMSWRQAPGKGLWVAIVSYDGN-KY 59
 QY 60 YADSVKGRFTISRDNSKNTLYIQMNSLRADTAIVYCARDFD---RYFDLWGRGLTVTVSSGG 118
 Db 60 YDEKFNKILGTVTSSSTAYMELSLASDSAVYVARGGRGLDWGAGTTLTVSSGG 119
 QY 119 GSGGGGGGGGSGGSSALFQ-PASVSGSGGSGITISCTGSDIGAVNYVSWYQYFGKAPK 177
 Db 120 GSGGGGGGGGSGGSDIQMTSSSFVSLGRVITCK-ASEDI--YNNLAWYQKQKGNAPR 176
 QY 178 LLIYDVNRRPSGISNRFSGSKGSDTASLTISGLQAEDEADYVCSFANSGLFPGGKTV 237
 Db 177 LLISGATSLTGVPSNRFSGSGSKDYTLSTISLTEDVATYVCCQVW-STRTFGGGLKLE 235
 QY 238 V 238
 Db 236 I 236

RESULT 4

Q8WUK1 PRELIMINARY; PRT; 613 AA.
 AC Q8WUK1;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC020240; AAH20240.1; -.
 DR PIR; P0120; P0120.
 DR PIR; S15590; S15590.
 DR InterPro; IPR007110; IG-Like.
 DR InterPro; IPR003006; IG_MHC.

InterPro; IPR003596; Ig_V.
PFam; PF00047; Ig; 5.
SMART; SM00406; IGV; 1.
PROSITE; PS00835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
Hypothetical protein_MHC; 3.
SEQUENCE 613 AA; 67296 MW; 60CTF5950671B315 CRC64;
Query Match 44.2%; Score 552.5; DB 4; Length 613;
Best Local Similarity 54.1%; Pred. No. 4.8e-35;
Matches 125; Conservative 19; Mismatches 44; Indels 43; Gaps 9;
2Y 1 QVQLQSGGGLVQPGGSLRLSCAASGFTSSVMSWVRQAPGKLEWAVIVDGSNKYY 60
2b 20 QVQLVESGGGVQPGSLRLSCAASGFTSSVMSWVRQAPGKLEWAVIVDGSNKYY 79
2Y 61 ADSVKGRTISRDNKNTLYLQNSLRADTAIVYCAR-----RYFDLWGRGLTVTVSS 115
2b 80 ADSVKGRTISRDNKNTLYLQNSLRADTAIVYCARDKWSEGVEFDWGGQTVTVSS 139
2Y 116 GGGSGGGGGGGGQSQALTPASVSGSPG--QSIITISCTGTSSDIGAYNV-----SW 167
2b 140 -----GSASAPTLPLVSCENSPDTSVAVGCL-----AQDFLPDSITFSW 181
2Y 168 YQVYGPGRKPLLIYDVNRPDSGISNRPFGSKSGDTASLTISG---LQADE 215
2b 182 --XYKNS-----DISS--TRGPPSVLRGGKYAATSQVLLPSKDVMOGTDE 223
RESULT 5
29UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035024; AAD56260.1; -.
DR HSP; P01772; 2PB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR PFam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON TER 113
FT NON TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;
Query Match 41.9%; Score 524; DB 4; Length 113;
Best Local Similarity 87.8%; Pred. No. 1e-33;
Matches 101; Conservative 5; Mismatches 7; Indels 2; Gaps 1;
QY 1 QVQLQSGGGLVQPGGSLRLSCAASGFTSSVMSWVRQAPGKLEWAVIVDGSNKYY 60
Db 1 EVQLVESGGGVQPGGSLRLSCAASGFTSSVMSWVRQAPGKLEWAVIRYDGSNKYY 60
QY 61 ADSVKGRTISRDNKNTLYLQNSLRADTAIVYCARDFDLWGRGLTVTVSS 115
Db 61 ADSVKGRTISRDNKNTLYLQNSLRADTAIVYCARDFDLWGRGLTVTVSS 113

RESULT 6
Q925S1 PRELIMINARY; PRT; 218 AA.
ID Q925S1
AC Q925S1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MRP5 (Fragment)
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after irradiation in mice";
RL World J. Gastroenterol. 6:709-717 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of the same strain";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80 (2001).
DR EMBL; AF240168; AAK4733.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR PFam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON TER 218
FT NON TER 218
SQ SEQUENCE 218 AA; 527E4FA8F7982817 CRC64;
Query Match 41.4%; Score 517.5; DB 11; Length 218;
Best Local Similarity 50.7%; Pred. No. 7.4e-33;
Matches 108; Conservative 35; Mismatches 63; Indels 7; Gaps 4;
QY 1 QVQLQSGGGLVQPGGSLRLSCAASGFTSSVMSWVRQAPGKLEWAVIVDGSNKYY 60
Db 3 QVQLQSGGGLVQPGGSLRLSCAASGFTSSVMSWVRQAPGKLEWAVIVDGSNKYY 62
QY 61 ADSVKGRTISRDNKNTLYLQNSLRADTAIVYCAR---DRYFDLWGRGLTVTVSSGG 117
Db 63 ABEFKGRFAFSLTSASTAYLQISLNKEDTATYFCMRWDYDGGPAYWGQGTTVTVSSGG 122
QY 118 GGGSGGGGGGGGQSQALTPQ--PASVSGSPGQSIITISCTGTSS--DIGAYNVYVSWYQYQPK 174
Db 123 GGGSGGGGGGGGQSDIVLTPQSPASLAVSLGQRATISCRASESDVDNIG--ISFMNWFQKQPKQ 181
QY 175 APKLLIYDVNRPDSGISNRPFGSKSGDTSASLTIT 207
Db 182 PPKLLIYAASKQSGGVPAGLLASGSGTDFSLNI 214
RESULT 7
Q9UL93 PRELIMINARY; PRT; 116 AA.
ID Q9UL93
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

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RP MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B.; Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9;1948-1953(1995).
DR EMBL; S80860; AAD14339.1; -.
DR HSSP; P01772; 2PB4.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0016489; F:immunoglobulin receptor activity; NAS.
DR GO; GO:0016086; P:cellular defense response (sensu Vertebrata); NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER
FT SEQUENCE 147 AA; 15768 MW; 3489FCAAA7BC925C CRC64;

Query Match 39.5%; Score 494; DB 4; Length 147;
Best Local Similarity 67.9%; Mism.No. 3,2e-31;
Matches 106; Conservative 8; Mismatches 22; Indels 20; Gaps 4

QY 1 QVQLCESGGVLVPGGGSLRLSCAASGFTSSYSSWVRQAPGKGLWAVISYDGSNKY 60
DB 1 QVHVESGGGVVPGKSLRLSCAASGFTSTYGSWVRQAPGKGLDWALISYDSTQY 60

QY 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD-RYF-----DLWGRT 109
DB 61 AGSVKGRFTISRDNSKNTLYLQMTSLRVEDTAVYYCAKDGNYPDSVGYVYAGIDYWGQT 120

QY 110 LVTSSGGGGGGGGGGGGGSGQSALQTPASVSGSPG 145
DB 121 LVTSS-----ASTKGPSVFLA-PSSKSTSG 147

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RESULT	10
Q9UL84	
ID	Q9UL84
IC	Q9UL84;
PRELIMINARY;	PRT; 122 AA.
DT	01-MAY-2000 (TRENBLrel. 13, Created)
DT	01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT	01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE	Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Carnivori;
NCBI TaxID=9606;	
OX	

1	EVQLVESGGGVQPGGSLRLSCAASGFTFDG	YAKHWVROAPKGLWVSLISGGGSIYY	60
2	ADSVKGRFTISRDNSKNTLYIQMNSLRAEDTA	VYICARDRY-----FDLWGRGTLVTVS	114
3	ADSVKGRFTISRDNSKNTLYIQMNSLRAEDTA	VYICAKGKVTIYDREDINGQGTMTVTS	120
4	115 S	115	
5	121 S	121	
6	121 S	121	
7	115 S	115	
8	121 S	121	
9	121 S	121	
10	115 S	115	
11	121 S	121	
12	121 S	121	
13	115 S	115	
14	121 S	121	
15	121 S	121	
16	115 S	115	
17	121 S	121	
18	121 S	121	
19	115 S	115	
20	121 S	121	
21	121 S	121	
22	115 S	115	
23	121 S	121	
24	121 S	121	
25	115 S	115	
26	121 S	121	
27	121 S	121	
28	115 S	115	
29	121 S	121	
30	121 S	121	
31	115 S	115	
32	121 S	121	
33	121 S	121	
34	115 S	115	
35	121 S	121	
36	121 S	121	
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55	115 S	115	
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57	121 S	121	
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96	121 S	121	
97	115 S	115	
98	121 S	121	
99	121 S	121	
100	115 S	115	
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102	121 S	121	
103	115 S	115	
104	121 S	121	
105	121 S	121	
106	115 S	115	
107	121 S	121	
108	121 S	121	
109	115 S	115	
110	121 S	121	
111	121 S	121	
112	115 S	115	
113	121 S	121	
114	121 S	121	
115	115 S	115	
116	121 S	121	
117	121 S	121	
118	1		

01-OCT-2003 (TREMBL1: 25, last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region

```

DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]_
RR SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RRL Clin. Immunol. Immunopathol. 87:184-192(1998).
RRL EMBL; AF035023; AADS6259.1; -.
DR PIR; S21205; S21205.
DR HSP; P01772; 2EB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON TER 1
FT NON TER 118
FT NON TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 38.8%; Score 484.5; DB 4; Length 118;
Best Local Similarity 81.2%; Pred.No.1.3e-30;
Matches 95; Conservative 8; Mismatches 11; Indels 3; Gaps 1;

QY 1 QVQLQESGGGLVPGGSLRLSCAASGFTSSYSMSWVRQAPEKGLEWVAISYDGSKYY 60
DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTSSYSMNWRQAPEKGLEWVSISTIIYY 60
QY 61 ADSVKGRFTISRDNKNTLYLNWSLRADTVAVYCAR--DRVFDLMRGTTVTVS 114
DB 61 ADSVKGRFTISRDNKNSLYLNWSLRADTVAVYCARGDSEAFDWGGTWTVTVS 117

RESULT 14
Q9UL72 PRELIMINARY; PRT; 118 AA.
AC Q9UL72;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DDT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DDT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
DE OS Homo sapiens (Human).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
DE NCBI_TaxID=9606;
DE RN [1]_
DE RR SEQUENCE FROM N.A.
DE RX MEDLINE=98277139; PubMed=9614934;
DE RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
DE RT Young D.C.;
DE RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
DE RRL Clin. Immunol. Immunopathol. 87:184-192(1998).
DE RRL EMBL; AF035042; AADS6278.1; -.
DR PIR; S21205; S21205.
DR HSP; P01772; 2EB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON TER 1
FT NON TER 118
FT NON TER 118
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 39.6%; Score 482.5; DB 4; Length 118;
Best Local Similarity 81.5%; Pred.No.1.9e-30;

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Matches 97; Conservative 7; Mismatches 10; Indels 5; Gaps 2
QY 1 QVQLQESGGGLVPGGSLRLSCAASGFTPSVYSMWVRQAPGKGLEWVAIVSYDGSNKYY 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTVSSNYMNWRQAPGKGLSVSV-TYSGGSYY 59
QY 61 ADSVKGRFTISRDNKNTIYLQWNSLRAEDTAVYCARDY----FQLWGRGTLVTSS 115
Db 60 ADSVKGRFTISRDNKNTIYLQWNSLRAEDTAFYCARDRGELFDYWGGLVTSS 118

RESULT 15
Q99KA4 PRELIMINARY; PRT; 487 AA.
ID Q99KA4
AC Q99KA4
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_taxID=10090;
RN [1]_taxID=10090;
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RR EMBL; BC004786; AAH04786.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB33077B CRC64;

Query Match 37.7%; Score 471; DB 11; Length 487;
Best Local Similarity 46.4%; Pred. No. 8, 8e-29;
Matches 111; Conservative 30; Mismatches 50; Indels 48; Gaps 9;

QY 1 QVQLQESGGGLVPGGSLRLSCAASGFTPSVYSMWVRQAPGKGLEWVAIVSYDGSNKYY 60
Db 20 EVQLVESGGGLVPGGSLRLSCAASGFTPSVYAMSVRQTPEKLEWVAIVSDGGSYY 79
QY 61 ADSVKGRFTISRDNKNTIYLQWNSLRAEDTAVYCARDY-----RVFDLWGRGLV 111
Db 80 PDNVKGRFTISRDNKNNIYLQVSHKSEDATAMYCARDMGSPYGGYRFDYWGQTII 139
QY 112 TVSSGGGGGGGGGGGSGSALTQTPASVSGSPGQSTITSC-----TGTSSDIGANYV 164
Db 140 TVSS-----ESARNPIYPLTLPALSSDP---VIIGLIHDYFFSGTMN----- 181
QY 165 VSWYQQYPGKAPKLLIYDYS--NRPSGINSRPSGSKSGDTSASLTISGLQAEADYVCS 221
Db 182 VTW-----GASGK-----DITVNFPPALA---SGGYTMSQLLPVACPGESEVKCS 228

Search completed: March 15, 2004, 07:27:20
Job time : 47 secs

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Search completed: March 15, 2004, 07:27:20
Job time : 47 secs

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% protein - protein search, using sw model

Run on: March 15, 2004, 07:25:43 ; Search time 17 Seconds
(without alignments)
732.045 Million cell updates/sec

Title: OS-09-620-955B-6
Perfect score: 1250
Sequence: 1 QVQLQESGGGLVQPGGSLRL.....CSSFANSGLPLFGGKTKVTVL 239

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	507.5	40.6	122	1 HV3G_HUMAN	P01768 homo sapien
2	488	39.0	112	1 HV2K_HUMAN	P04209 homo sapien
3	478	38.2	119	1 HV3J_HUMAN	P01770 homo sapien
4	472	37.8	121	1 HV3J_HUMAN	P01771 homo sapien
5	468.5	37.5	111	1 HV2B_HUMAN	P01705 homo sapien
6	465.5	37.2	111	1 HV2A_HUMAN	P01704 homo sapien
7	462.5	37.0	122	1 HV3H_HUMAN	P01769 homo sapien
8	454.5	36.4	111	1 HV2D_HUMAN	P01707 homo sapien
9	453.5	36.3	126	1 HV2K_HUMAN	P01772 homo sapien
10	452.5	36.2	114	1 HV3B_HUMAN	P01763 homo sapien
11	452	36.2	117	1 HV3C_HUMAN	P01764 homo sapien
12	449.5	36.0	111	1 HV2H_HUMAN	P01711 homo sapien
13	444	35.5	115	1 HV3D_HUMAN	P01765 homo sapien
14	443	35.4	115	1 HV3F_HUMAN	P01767 homo sapien
15	439.5	35.2	111	1 HV2F_HUMAN	P01709 homo sapien
16	437.5	35.0	119	1 HV3M_HUMAN	P01774 homo sapien
17	435.5	34.8	111	1 HV2G_HUMAN	P01710 homo sapien
18	435.5	34.8	119	1 HV3N_HUMAN	P01775 homo sapien
19	435.5	34.8	136	1 HV16_MOUSE	P01783 mus musculu
20	434.5	34.8	109	1 HV2E_HUMAN	P01708 homo sapien
21	433.5	34.7	116	1 HV05_CARAU	P19181 carassius a
22	432.5	34.6	116	1 HV3T_HUMAN	P01781 homo sapien
23	430	34.4	119	1 HV3L_HUMAN	P01773 homo sapien
24	430	34.4	120	1 HV3E_HUMAN	P01776 homo sapien
25	428.5	34.3	117	1 HV3O_HUMAN	P01778 homo sapien
26	425	34.0	110	1 HV2J_HUMAN	P01713 homo sapien
27	423.5	33.9	111	1 HV2C_HUMAN	P01706 homo sapien
28	422.5	33.8	122	1 HV3A_HUMAN	P01762 homo sapien
29	421.5	33.7	119	1 HV3U_HUMAN	P01808 mus musculu
30	417.5	33.4	120	1 HV3U_HUMAN	P01782 homo sapien
31	415.5	33.2	111	1 LV2I_MOUSE	P01712 homo sapien
32	414.5	33.2	119	1 HV37_MOUSE	P01807 mus musculu
33	414.5	33.2	122	1 HV20_MOUSE	P01789 mus musculu

34	414	33.1	117	1 HV02_CANFA	P01785 canis famil
35	414	33.1	123	1 HV18_MOUSE	P01787 mus musculu
36	414	33.1	123	1 HV19_MOUSE	P01788 mus musculu
37	414	33.1	123	1 HV22_MOUSE	P01791 mus musculu
38	413	33.0	115	1 HV32_MOUSE	P01801 mus musculu
39	413	33.0	123	1 HV25_MOUSE	P01784 mus musculu
40	411	32.9	113	1 HV30_MOUSE	P01789 mus musculu
41	410.5	32.8	114	1 HV01_CANFA	P01782 canis famil
42	410	32.8	123	1 HV23_MOUSE	P01782 mus musculu
43	409	32.7	123	1 HV01_RAT	P01805 rattus norv
44	408	32.6	123	1 HV24_MOUSE	P01793 mus musculu
45	407.5	32.6	122	1 HV21_MOUSE	P01790 mus musculu

ALIGNMENTS

RESULT 1
HV3G_HUMAN
ID HV3G_HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain;
RT location of a possible JH segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC -!- PATIENT WITH MACROGLOBULINEMIA.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02051; M3HMAN.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyridolone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C3 CRC64;

Query Match 40.6%; Score 507.5; DB 1; Length 122;
Best Local Similarity 77.9%; Pred. No. 8.7e-32;
Matches 95; Conservative 13; Mismatches 7; Indels 7; Gaps 1;
QY 1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSYNSWVRQAPGKLEWVAIVSYDGSNKYY 60
Db 1 QVELVESGGGVVQPSRLSLRSCAASGFTFSYNSAMHWVRQPPGKLEWVAIVSYEGBBKYY 60
QY 61 ADSVKGRFTISRDNSKNTLYQMNSLRAEDEVAVYYCARD-----RYFDLWGRGLTAV 113
Db 61 ABSVKGRTISRDNSKNTLYQMNSLRAEDEVAVYYCARDRLYGBYAFNYWGGLTAV 120
QY 114 SS 115
Db 121 SS 122

RESULT 2

LV2K HUMAN
ID LV2K HUMAN STANDARD; PRT; 112 AA.
AC P04209;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-II region NTG-84.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=85204383; PubMed=3922791;
RA Tonsike H, Kamekani F, Hoshi A, Shinoda T, Isobe T;
RT "Amino acid sequence of an amyloidogenic Bence Jones protein in myeloma-associated systemic amyloidosis.";
RL FEBS Lett. 185:139-141(1985).
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN ISOLATED FROM AN INDIVIDUAL WITH MYELOMA-ASSOCIATED SYSTEMIC AMYLOIDOSIS.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01971; L2HUNG.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Amyloid; Bence-Jones protein.
FT DOMAIN 1 102
FT DISULFID 22 90
FT NON TER 112 112
FT SEQUENCE 112 AA; 11581 MW; 988PF363AE1E4F3 CRC64;
Query Match 39.0%; Score 488; DB 1; Length 112;
Best Local Similarity 84.7%; Pred. No. 2.3e-30;
Matches 94; Conservative 11; Mismatches 4; Indels 2; Gaps 1;
QY 131 QSALTQPSVSGSPQSTISCTGTSIDGAYNVYVYQYQPKAKPLIYDYNRPSCI 190
Db 1 QSALTQPSVSGSPQSTISCTGTSIDGAYNVYVYQYQPKAKPLIYDYNRPSCI 60
QY 191 SNRFGSKSGTASLTISGLQAEADYCYCSF--ANSGLFGGKTVYL 239
Db 61 SNRFGSKSGTASLTISGLQAEADYCYCSFTTNSRAVFGGKLSVL 111
RESULT 3
HV3J HUMAN
ID HV3J HUMAN STANDARD; PRT; 119 AA.
AC P01770;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region NIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H, Hilschmann N;
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [2]
RP DISULFIDE BOND.

MEDLINE=77070267; PubMed=1002129;
RA Dreker L, Schwarz J, Reichel W, Hilschmann N;
RT "Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA PROTEIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A91668; GIHUNI.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Pyrrrolidone carboxylic acid.
FT DOMAIN 1 112
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT NON TER 119 119
FT SEQUENCE 119 AA; 13242 MW; C9693SA6E5E165B CRC64;
Query Match 38.2%; Score 478; DB 1; Length 119;
Best Local Similarity 77.3%; Pred. No. 1.4e-29;
Matches 92; Conservative 12; Mismatches 11; Indels 4; Gaps 1;
QY 1 QVQLQSGGGLVQPGGSLRLSCAASGFTPSYSMGVRQAPGKLEWAVYSYDGSNKYY 60
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTPSYTHWVRQAPGKLEWAVMSYBGBRHY 60
QY 61 ADSVKGRTISRNSKNTLYLQNSLRADTVYICARDR----YFDLWGRGLTVVSS 115
Db 61 ADSVNGRFTISRNSKNTLYLQNSLRADTVYICARDTAMFFAHGQGLTVVSS 119
RESULT 4
HV3J HUMAN
ID HV3J HUMAN STANDARD; PRT; 121 AA.
AC P01771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region HIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=79124695; PubMed=420800;
RA Chiu Y.-Y. H., Lopez de Castro J.A., Poljak R.J.;
RT "Amino acid sequence of the VH region of human myeloma cryoimmunoglobulin Igg Hil.";
RL Biochemistry 18:553-560(1979).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA PROTEIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02054; GIHUEL.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Pyrrrolidone carboxylic acid.

T DOMAIN 1 112 IG-LIKE.
T MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
T NON TER 121 121
Q SEQUENCE 121 AA; 13566 MW; 480FC53610EP5DAB CRC64;

Query Match 37.8%; Score 472; DB 1; Length 121;
Best Local Similarity 75.2%; Pred. No. 4e-29;
Matches 91; Conservative 9; Mismatches 15; Indels 6; Gaps 1;

1 QVQLQSGGGLVQPGSLRLSCAASGFTFSYSGMWVROAPKGLWVAVISYDGSNKYY 60
1 QVQLVAGGQVQVQGRSLRLSCAASGFTFSYSGMWVROAPKGLWVAVISYDGSNKYY 60
61 ADSVKGRFTISRDNSKNTLYLQWNSLRDEDTAVVYCARDR-----YFDLWGRGLTVTS 114
61 GDSVKGRFTISRDNSKNTLYLQWNSLRDEDTAVVYCARDPDILTAFFDYWGQGLVTVS 120
115 S 115
121 S 121

RESULT 5
LV2B_HUMAN STANDARD; PRT; 111 AA.
ID LV2B_HUMAN
AC P01705;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-II region NEI.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
SEQUENCE.
MEDLINE=72233223; PubMed=5043326;
RA Garver P.A., Hirschmann M.;
RT "The primary structure of a monoclonal human lambda-type
immunoglobulin L-chain of subgroup II (Bence-Jones protein NEI).";
RL Sur. J. Biochem. 26:10-32(1972).
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01970; L2HUNI.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein;
KW Pyrrrolidone carboxylic acid.
FT DOMAIN 1 106 IG-LIKE.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .).
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11591 MW; AD6D156584D087EB CRC64;

Query Match 37.5%; Score 468.5; DB 1; Length 111;
Best Local Similarity 81.8%; Pred. No. 6.7e-29;
Matches 90; Conservative 11; Mismatches 8; Indels 1; Gaps 1;

131 QSALTQPASVSGSPGSGITISCTGSSDIGAYNVSWYQYQPGKPKLLIYDVSNRPSGI 190
1 QSALTQPASVSGSPGSGITISCTGSSDIGAYNVSWYQYQPGKPKLLIYDVSNRPSGV 60
191 SNRFGSKSGDTSALTSIGLQAEDEADYCCSFANSGPLFGGGTKVTVL 239
61 SNRFGSKSGKTSALTSIGLQAEDEADYCCSYAGNSTRVFGGTRTVTL 110

RESULT 6
LV2A_HUMAN STANDARD; PRT; 111 AA.
ID LV2A_HUMAN
AC P01704;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-II region TOG.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
SEQUENCE.
MEDLINE=80048495; PubMed=500108;
RA Nabeshima Y., Ikenaka T.;
RT "Primary structure of cryo Bence-Jones protein (Tog) from the urine
of a patient with IGD myeloma.";
RL Mol. Immunol. 16:439-444(1979).
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01969; L2HUTG.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein;
KW Pyrrrolidone carboxylic acid.
FT DOMAIN 1 100 IG-LIKE.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11713 MW; PD20AEF4CE5364E2 CRC64;

Query Match 37.2%; Score 465.5; DB 1; Length 111;
Best Local Similarity 80.9%; Pred. No. 1.1e-28;
Matches 89; Conservative 14; Mismatches 6; Indels 1; Gaps 1;

131 QSALTQPASVSGSPGSGITISCTGSSDIGAYNVSWYQYQPGKPKLLIYDVSNRPSGI 190
1 QSALTQPASVSGSPGSGITISCTGSSDIGAYNVSWYQYQPGKPKLLIYDVSNRPSGV 60
191 SNRFGSKSGDTSALTSIGLQAEDEADYCCSFANSGP-LFGGGTKVTVL 239
61 SNRFGSKSGKTSALTSIGLQAEDEADYCCSYRTSGTIIFGGTYTVTL 110

RESULT 7
HV3H_HUMAN STANDARD; PRT; 122 AA.
ID HV3H_HUMAN
AC P01769;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region GA.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
SEQUENCE.
MEDLINE=74175307; PubMed=4208843;
RA Florent G., Lehman D., Putnam F.W.;
RT "The switch point in mu heavy chains of human IgM immunoglobulins.";
RL Biochemistry 13:2482-2498(1974).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S

CC MACROGLOBULIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02052; M3HUGA.
DR HSSP: P01772; 2FB4.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Pyridone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13166 MW; 745B5959E84100A CRC64;

Query Match 37.0%; Score 462.5; DB 1; Length 122;
Best Local Similarity 68.9%; Pred. No. 2.1e-28;
Matches 84; Conservative 19; Mismatches 12; Indels 7; Gaps 1;

QY 1 OVQLQSGGLVQPGSLRLSCAASGFTFSYSSMSVWQAPKGLWVAVISYDGSNYY 60
DB 1 QVZLVZSGGAVZPGSLRLSCAASGFTFSYAMHWVQAPKGLZMLSVISYBGBZYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQNSLRARDEAVYICARDY-----FDLWGRGTLVTV 113
DB 61 AASVKGRFTISRDBSKBTWYLEWNSLRARNTAVYICARSGIALGSAVAGTQVWGZGLTVTI 120

QY 114 SS 115
DB 121 SS 122

RESULT 8
LV2D HUMAN
ID LV2D HUMAN STANDARD; PRT; 111 AA.
AC P01707;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda chain V-II region TRC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=80114123; PubMed=118915;
RA Scholz R., Yang C., Hilschmann N.;
RT "Rule of antibody structure. Primary structure of a human monoclonal IgA1-immunoglobulin (myeloma protein Trol). VI. Amino acid sequence of the L-chain, lambda-type, subgroup II.";
RL Hoppe-Seyler's Z. Physiol. Chem. 360:1903-1918 (1979).
CC -1- MISCELLANEOUS. THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A01973; L2HUTR.
DR HSSP: P01709; 2MCG.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Pyridone carboxylic acid.
FT DOMAIN 1 106 IG-LIKE
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11561 MW; 99DC457A12E9F6E1 CRC64;

Query Match 36.4%; Score 454.5; DB 1; Length 111;
Best Local Similarity 78.2%; Pred. No. 7.6e-28;
Matches 86; Conservative 13; Mismatches 10; Indels 1; Gaps 1;

QY 131 QSALTQPASVSGSPGQITISCTSSDYGANNVSVYQYQPKAPKLLIYDVNSPGL 190
DB 1 QSALTQPRSVSGSPGQVTISCTSSDVGAYNSVYQYQPKAPKLMIFDVKRPSGV 60

QY 191 SNRPSGSGDGTASLTISGLQAEADYCYSSPANS-GPLFGGQTKVTVL 239
DB 61 PDLRSGSGDGTASLTISGLRADDEADYCCSVAGRYSVIFGGTKLTVL 110

RESULT 9
HV3K HUMAN
ID HV3K HUMAN STANDARD; PRT; 126 AA.
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E. Jung H.-D. Palm W.; Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747 (1983).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marquart M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A and 1.0-A resolution.";
RL J. Mol. Biol. 141:369-391 (1980).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02055; GIHUKL.
DR PDB: 2FB4; 12-JUL-89.
DR PDB: 2IG2; 12-JUL-89.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS0835; IG LIKE; 1.
KW Immunoglobulin V region; 3D-structure; Pyridone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT DISULFID 105 110
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 25
FT STRAND 29 31
FT HELIX 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT STRAND 58 60
FT STRAND 62 64
FT HELIX 62 65
FT STRAND 65 67
FT TURN 66 67
FT STRAND 68 73
FT TURN 74 77


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FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 116
FT STRAND 120 124
FT NON TER 126 126
SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

Query Match 36.3%; Score 453.5; DB 1; Length 126;
Best Local Similarity 71.4%; Pred. No. 1e-27;
Matches 90; Conservative 12; Mismatches 13; Indels 11; Gaps 1;

QY 1 QVQLQESGGGLVPGGSLRLSCAASGFTFSYSSMSWVRQAPGKGLWEWAVISYDGSNKYY 60
DB 1 QVQLVESGGGVQPGSLRLSCSSSGIFESSYAMWVRQAPGKGLWEWAVIWDGSDQHY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARDRYF-----DLWGRGT 109
DB 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARDRYF-----DLWGRGT 109
QY 110 LVTVSS 115
DB 121 PVTVSS 126

RESULT 10
HV3B_HUMAN
ID HV3B_HUMAN STANDARD; PRT; 114 AA.
AC P01763;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-III region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=83273707; PubMed=6410398;
RX Medline=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IGM
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33."
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02046; M3HUWE.
DR HSP; P01772; 2PBA.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR WALDENSTROM'S MACROGLOBULINEMIA.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT DOMAIN 20 >117 IG-LIKE.
FT NON TER 117 117
SQ SEQUENCE 114 AA; 12256 MW; D88294FB418A07B7 CRC64;

Query Match 36.2%; Score 452.5; DB 1; Length 114;
Best Local Similarity 76.5%; Pred. No. 1e-27;
Matches 88; Conservative 13; Mismatches 13; Indels 1; Gaps 1;

QY 1 QVQLQESGGGLVPGGSLRLSCAASGFTFSYSSMSWVRQAPGKGLWEWAVISYDGSNKYY 60
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DB 1 QVQLVDSGGGLVPGGSLRLSCASGFTFSANDMWVRQAPGKGLWLSPTFGSGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARDRYFDLWGRGTLVTSS 115
DB 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCARDRYFDLWGRGTLVTSS 114

RESULT 11
HV3C_HUMAN
ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-III region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81101090; PubMed=6450418;
RA Matthysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RT heavy chain variable region."
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00236; AAA53516.1; -
DR EMBL; M35415; AAA58735.1; -
DR PIR; A02047; H3HU28.
DR PDB; 1HCU; 23-DEC-99.
DR Genew; HGNC:5545; IGHV@.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT DOMAIN 20 >117 IG-LIKE.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12592 MW; E826733F1A3CB0F1 CRC64;

Query Match 36.2%; Score 452; DB 1; Length 117;
Best Local Similarity 87.8%; Pred. No. 1.2e-27;
Matches 86; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLQESGGGLVPGGSLRLSCAASGFTFSYSSMSWVRQAPGKGLWEWAVISYDGSNKYY 60
DB 20 EQVLQESGGGLVPGGSLRLSCAASGFTFSYSSMSWVRQAPGKGLWEWAVISYDGSNKYY 79
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAR 98
DB 80 GDSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAK 117

RESULT 12
LV2H_HUMAN
ID LV2H_HUMAN STANDARD; PRT; 111 AA.
```

AC P01711;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain V-II region VII.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=71215142; PubMed=5087637;
 RA Festschlag H., Hilschmann N.;
 RT "Structural rule of antibodies. Complete primary structure of a
 RT monoclonal immunoglobulin L chain of the lambda type, subgroup II
 RT (Bence Jones protein VII).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 352:859-877(1971).
 CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A01977; L2HUVL.
 DR HSSP; P01709; 2MCG.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 100
 FT DISULFID 22 90
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 11445 MW; 3913736B3EF367E0 CRC64;
 Query Match 36.0%; Score 449.5; DB 1; Length 111;
 Best Local Similarity 79.8%; Pred. No. 1.8e-27;
 Matches 87; Conservative 12; Mismatches 9; Indels 1; Gaps 1;
 YQ 132 SALTQASVSGSGPSSITISCTGTSDDICAYNYSWYQYQFGKAPKLLIYDVSNRPSGIS 191
 Db 2 SALTQASVSGSLQGSITISCTGTSDDVGGYVSWFQHPGTAPKLIIEVNRPSGV 61
 YQ 192 NRPFSKSGDTSATISGLQAEDEADYVCSFANSGP-LFGGKTKVTL 239
 Db 62 DRPFSKGSANTASLTISGLQAEDEADYVCSYTSNSVVFPGGKTLVL 110
 RESULT 13
 HV3D HUMAN
 ID HV3D HUMAN STANDARD; PRT; 115 AA.
 AC P01765;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region TII.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=78005528; PubMed=409716;
 RA Wang A.-C., Wang I.-Y., Fudenberg H.H.;
 RT "Immunoglobulin structure and genetics. Identity between variable
 RT regions of a mu and a gamma2 chain.";
 RL J. Biol. Chem. 252:7192-7199(1977).
 CC -!- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
 CC OF IGM AND IG22 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
 CC GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
 CC IDENTICAL.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02048; H3HUTL.

DR HSSP; P01772; 2PB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 DR Immunoglobulin V region.
 KW DOMAIN 1 108
 FT NON TER 115 115
 FT NON TER 115 115
 SQ SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;
 Query Match 35.5%; Score 444; DB 1; Length 115;
 Best Local Similarity 73.9%; Pred. No. 4.8e-27;
 Matches 88; Conservative 10; Mismatches 13; Indels 8; Gaps 2;
 YQ 1 OVQLQESGGGVQPGGSLRLSCAASGFTSSYMSVWRQAPGKLEWAVISYDGSNKYY 60
 Db 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYVMSWRQAPGKLEWAVISYDGSNKYY 60
 YQ 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDR---YFDLMGRGLTVTVSS 115
 Db 61 ABSVKGRFTISRDNKNT---NNSLRAEDTAVYYCAKGVSAFYFYMGZGLTVTVSS 115
 RESULT 14
 HV3F HUMAN
 ID HV3F HUMAN STANDARD; PRT; 115 AA.
 AC P01767;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region BUT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=78137069; PubMed=416441;
 RA Torano A., Putnam F.W.;
 RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
 RT IgA2 immunoglobulin of the A2m (2) allotype.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
 CC -!- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M (2) ALLOTYPES, C
 CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02050; A2HUBU.
 DR HSSP; P01789; 1MCP.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 DR Immunoglobulin V region.
 KW DOMAIN 1 111
 FT NON TER 115 115
 FT NON TER 115 115
 SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCF4 CRC64;
 Query Match 35.4%; Score 443; DB 1; Length 115;
 Best Local Similarity 75.0%; Pred. No. 5.8e-27;
 Matches 87; Conservative 13; Mismatches 14; Indels 2; Gaps 2;
 YQ 1 OVQLQESGGGVQPGGSLRLSCAASGFTSSYMSVWRQAPGKLEWAVISYDGSNKYY 60
 Db 1 EVQLVETGGGLIQQGSLRLSCAASGFTVSBHSMVWRQAPGKLEWAVISYDGSNKYY 59
 YQ 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDR---YFDLMGRGLTVTVSS 115

FT	DISULFID	22	5	50	BT
FT	STRAND	5	5		
FT	STRAND	10	12		
FT	STRAND	18	23		
FT	STRAND	26	32		
FT	TURN	26	32		
FT	STRAND	36	40		
FT	TURN	42	43		